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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:06:39 ; Search time 13 Seconds
(without alignments)
67.365 Million cell updates/sec

Title: US-09-674-913a-1
Perfect score: 99
Sequence: 1 NVPGERMGRGRTSSKELA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 48531

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published.Applications_AA:*
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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	32	32.3	19	10	US-09-864-761-47043
5	31	31.3	20	10	US-09-864-761-43265
6	31	31.3	20	10	US-09-876-204-3
7	31	31.3	23	10	US-09-955-518-14
8	29	29.3	9	10	US-09-845-667-22
9	29	29.3	10	10	US-09-867-852-95
10	29	29.3	17	9	US-10-056-407-23
11	29	29.3	19	10	US-09-847-519A-3
12	29	29.3	23	10	US-09-864-761-46793
13	29	29.3	25	10	US-09-864-761-38863
14	28.5	28.8	25	8	US-08-424-550B-242
15	28	28.3	14	9	US-10-056-407-26
16	28	28.3	21	10	US-09-775-925-3
17	27	27.3	8	10	US-09-845-667-35
18	27	27.3	11	9	US-10-108-795-26
19	27	27.3	11	10	US-09-845-667-1

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24	26	26.3	7	10	US-09-845-667-45	Sequence 45, Appl
25	26	26.3	12	9	US-10-012-756-19	Sequence 19, Appl
26	26	26.3	17	10	US-09-864-761-40855	Sequence 40855, A
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249	21	21.2	10	10	US-09-810-310-21	Sequence 21, Appl	322	21	21.2	21	9	US-09-974-879-776	Sequence 276, App
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251	21	21.2	11	10	US-09-873-676-17	Sequence 17, Appl	324	21	21.2	21	10	US-09-864-761-35353	Sequence 35353, A
252	21	21.2	11	10	US-09-839-743-22	Sequence 22, Appl	325	21	21.2	21	10	US-09-864-761-38713	Sequence 38713, A
253	21	21.2	11	12	US-10-007-761-69	Sequence 69, Appl	326	21	21.2	21	10	US-09-864-761-39245	Sequence 39245, A
254	21	21.2	11	12	US-09-981-876-257	Sequence 257, App	327	21	21.2	21	10	US-09-864-761-41061	Sequence 41061, A
255	21	21.2	12	9	US-09-962-955c-31	Sequence 31, Appl	328	21	21.2	21	10	US-09-853-830-63	Sequence 41, Appl
256	21	21.2	12	9	US-09-148-545-257	Sequence 257, App	329	21	21.2	21	10	US-09-853-830-85	Sequence 85, Appl
257	21	21.2	12	9	US-09-903-412-118	Sequence 118, App	330	21	21.2	21	10	US-09-873-106b-22	Sequence 22, Appl
258	21	21.2	12	9	US-09-791-389-172	Sequence 172, App	331	21	21.2	21	10	US-09-864-761-42058	Sequence 39245, A
259	21	21.2	12	9	US-09-791-393-172	Sequence 172, App	332	21	21.2	21	12	US-10-016-481-7	Sequence 41061, A
260	21	21.2	12	9	US-09-918-873-23	Sequence 23, Appl	333	21	21.2	22	9	US-09-765-644a-33	Sequence 76, App
261	21	21.2	12	10	US-09-096-749a-118	Sequence 118, App	334	21	21.2	22	10	US-09-765-301-33	Sequence 33, Appl
262	21	21.2	13	9	US-09-291-925a-7	Sequence 7, Appl1	335	21	21.2	22	10	US-09-864-761-36540	Sequence 36540, A
263	21	21.2	13	9	US-09-791-389-164	Sequence 164, App	336	21	21.2	22	10	US-09-864-761-37167	Sequence 37167, A
264	21	21.2	13	9	US-09-791-393-164	Sequence 164, App	337	21	21.2	22	10	US-09-864-761-42058	Sequence 42058, A
265	21	21.2	13	10	US-09-873-637-6	Sequence 6, Appl1	338	21	21.2	22	10	US-09-864-761-43526	Sequence 39245, A
266	21	21.2	13	10	US-09-873-676-12	Sequence 12, Appl	339	21	21.2	22	12	US-09-864-761-46463	Sequence 46463, A
267	21	21.2	13	10	US-09-791-378-252	Sequence 252, App	340	21	21.2	22	12	US-10-013-036-5	Sequence 5, Appl1
268	21	21.2	13	10	US-09-071-838-34	Sequence 34, Appl	341	21	21.2	22	12	US-10-013-036-6	Sequence 6, Appl1
269	21	21.2	14	9	US-09-291-925a-5	Sequence 5, Appl1	342	21	21.2	22	12	US-10-013-036-8	Sequence 8, Appl1
270	21	21.2	14	10	US-09-935-682-44	Sequence 44, Appl	343	21	21.2	22	12	US-10-013-036-9	Sequence 9, Appl1
271	21	21.2	15	9	US-09-927-436-8	Sequence 8, Appl1	344	21	21.2	23	12	US-09-809-423a-29	Sequence 29, Appl
272	21	21.2	15	9	US-10-001-938-20	Sequence 20, Appl	345	21	21.2	23	9	US-09-991-548-11	Sequence 11, Appl
273	21	21.2	15	10	US-09-810-310-31	Sequence 31, Appl	346	21	21.2	23	10	US-09-864-761-40102	Sequence 40102, A
274	21	21.2	15	10	US-09-808-037-23	Sequence 23, Appl	347	21	21.2	23	10	US-09-864-761-42131	Sequence 42131, A
275	21	21.2	15	10	US-09-893-348-29	Sequence 29, Appl	348	21	21.2	23	10	US-09-864-761-42131	Sequence 42131, A
276	21	21.2	15	12	US-10-041-030-16	Sequence 16, Appl	349	21	21.2	23	10	US-09-788-632a-105	Sequence 105, App
277	21	21.2	16	10	US-09-842-164-7	Sequence 7, Appl1	350	21	21.2	24	9	US-09-974-879-457	Sequence 457, App
278	21	21.2	17	10	US-09-765-527-6	Sequence 6, Appl1	351	21	21.2	24	10	US-09-974-879-458	Sequence 488, App
279	21	21.2	17	10	US-09-864-761-41554	Sequence 41554, A	352	21	21.2	24	10	US-09-804-674-7	Sequence 7, Appl1
280	21	21.2	18	9	US-10-029-009-16	Sequence 16, Appl	353	21	21.2	24	10	US-09-864-761-47573	Sequence 47573, A
281	21	21.2	18	9	US-10-117-846-21	Sequence 21, Appl	354	21	21.2	25	9	US-09-875-494-4	Sequence 4, Appl1
282	21	21.2	18	9	US-09-864-761-35334	Sequence 35334, A	355	21	21.2	25	9	US-09-774-639-263	Sequence 263, App
283	21	21.2	18	10	US-09-864-761-43785	Sequence 43785, A	356	21	21.2	25	10	US-09-837-969a-54	Sequence 54, Appl
284	21	21.2	19	9	US-10-001-887-110	Sequence 110, App	357	21	21.2	25	10	US-09-837-969a-61	Sequence 61, Appl
285	21	21.2	19	9	US-10-029-009-28	Sequence 28, Appl	358	21	21.2	25	10	US-09-864-761-36891	Sequence 36891, A
286	21	21.2	19	9	US-10-117-846-30	Sequence 30, Appl	359	21	21.2	25	10	US-09-864-761-39663	Sequence 39663, A
287	21	21.2	19	9	US-10-117-846-32	Sequence 32, Appl	360	21	21.2	25	10	US-09-864-761-39667	Sequence 39667, A
288	21	21.2	19	9	US-10-117-846-34	Sequence 34, Appl	361	21	21.2	25	10	US-09-864-761-40572	Sequence 40572, A
289	21	21.2	19	9	US-10-018-103a-13	Sequence 13, Appl	362	21	21.2	25	10	US-09-841-321a-54	Sequence 54, Appl
290	21	21.2	19	10	US-09-799-875-26	Sequence 26, Appl	363	21	21.2	25	10	US-09-841-321a-61	Sequence 61, Appl
291	21	21.2	19	10	US-09-864-761-36523	Sequence 36523, A	364	21	21.2	25	10	US-09-974-879-456	Sequence 456, App
292	21	21.2	19	10	US-09-899-376-3	Sequence 3, Appl1	365	21	21.2	25	10	US-09-864-761-41024	Sequence 41024, A
293	21	21.2	19	10	US-09-308-150-1	Sequence 1, Appl1	366	21	21.2	24	10	US-09-030-619-213	Sequence 213, App
294	21	21.2	19	10	US-09-308-150-12	Sequence 12, Appl	367	20.5	20.7	24	10	US-09-864-761-35141	Sequence 35141, A
295	21	21.2	19	10	US-09-308-150-13	Sequence 13, Appl	368	20.5	20.7	24	10	US-09-917-340-2	Sequence 2, App
296	21	21.2	19	10	US-09-308-150-14	Sequence 14, Appl	369	20	20.2	6	9	US-10-007-270-33	Sequence 33, Appl
297	21	21.2	20	9	US-09-954-433-1	Sequence 1, Appl1	370	20	20.2	7	9	US-09-229-173-31	Sequence 31, App
298	21	21.2	20	9	US-09-984-245-305	Sequence 305, App	371	20	20.2	7	9	US-09-884-767a-112	Sequence 162, App
299	21	21.2	20	9	US-09-973-025-66	Sequence 66, Appl	372	20	20.2	7	9	US-10-084-832-1	Sequence 1, Appl1
300	21	21.2	20	9	US-09-899-303-66	Sequence 66, Appl	373	20	20.2	8	10	US-09-767-870-14	Sequence 14, Appl
301	21	21.2	20	9	US-09-988-462-75	Sequence 75, Appl	374	20	20.2	9	9	US-09-835-853-12	Sequence 12, Appl
302	21	21.2	20	10	US-09-864-761-47004	Sequence 47004, A	375	20	20.2	9	10	US-09-835-853-13	Sequence 15, Appl
303	21	21.2	20	10	US-09-864-761-48427	Sequence 48427, A	376	20	20.2	9	10	US-09-832-382-13	Sequence 13, Appl
304	21	21.2	20	10	US-09-735-705-242	Sequence 242, App	377	20	20.2	9	10	US-09-946-175-112	Sequence 12, Appl
305	21	21.2	20	10	US-09-735-705-245	Sequence 245, App	378	20	20.2	9	10	US-09-779-308-68	Sequence 611, App
306	21	21.2	20	10	US-09-735-705-246	Sequence 246, App	379	20	20.2	10	9	US-09-955-732-16	Sequence 16, Appl
307	21	21.2	20	10	US-09-735-705-247	Sequence 247, App	380	20	20.2	10	9	US-09-812-485a-40	Sequence 40, Appl
308	21	21.2	20	10	US-09-735-705-367	Sequence 367, App	381	20	20.2	10	9	US-09-899-046-219	Sequence 219, App
309	21	21.2	20	10	US-09-735-705-382	Sequence 382, App	382	20	20.2	10	9	US-09-899-046-220	Sequence 220, App
310	21	21.2	20	10	US-09-918-063-51	Sequence 51, Appl	383	20	20.2	10	9	US-09-899-046-221	Sequence 221, App
311	21	21.2	20	10	US-09-993-844-58	Sequence 58, Appl	384	20	20.2	10	9	US-09-878-281-219	Sequence 219, App

385	20	20.2	10	9	US-09-878-281-220	Sequence 220, App	458	20	20.2	18	10	US-09-864-761-42961	Sequence 42961, A
386	20	20.2	10	9	US-09-878-281-221	Sequence 221, App	459	20	20.2	18	10	US-09-864-761-44827	Sequence 44827, A
387	20	20.2	10	10	US-09-748-114-3	Sequence 3, Appl	460	20	20.2	19	9	US-10-038-612-113	Sequence 113, App
388	20	20.2	11	9	US-09-774-639-202	Sequence 202, App	461	20	20.2	19	9	US-09-812-485A-38	Sequence 38, Appl
389	20	20.2	11	10	US-09-894-018-160	Sequence 160, App	462	20	20.2	19	9	US-09-794-517-8	Sequence 8, Appl
390	20	20.2	11	10	US-09-984-056-6	Sequence 6, Appl	463	20	20.2	19	9	US-10-018-103A-10	Sequence 10, Appl
391	20	20.2	11	10	US-09-984-057-6	Sequence 6, Appl	464	20	20.2	19	10	US-09-864-761-38815	Sequence 38815, A
392	20	20.2	12	8	US-08-424-550B-429	Sequence 429, App	465	20	20.2	19	10	US-09-864-761-48146	Sequence 48146, A
393	20	20.2	12	9	US-09-981-876-266	Sequence 266, App	466	20	20.2	19	10	US-09-308-150-2	Sequence 2, Appl
394	20	20.2	12	9	US-10-094-679-7	Sequence 7, Appl	467	20	20.2	19	10	US-09-308-150-6	Sequence 6, Appl
395	20	20.2	12	9	US-09-983-802-501	Sequence 501, App	468	20	20.2	19	10	US-09-308-150-7	Sequence 7, Appl
396	20	20.2	12	9	US-09-148-545-266	Sequence 266, App	469	20	20.2	20	9	US-10-038-612-65	Sequence 65, Appl
397	20	20.2	12	10	US-09-748-114-2	Sequence 2, Appl	470	20	20.2	20	9	US-09-736-457-1835	Sequence 1835, App
398	20	20.2	12	12	US-10-057-113-18	Sequence 18, Appl	471	20	20.2	20	9	US-09-902-941-1835	Sequence 1835, App
399	20	20.2	12	12	US-10-057-113-19	Sequence 19, Appl	472	20	20.2	20	9	US-10-074-257-10	Sequence 10, Appl
400	20	20.2	12	12	US-10-057-113-20	Sequence 20, Appl	473	20	20.2	20	9	US-10-074-257-11	Sequence 11, Appl
401	20	20.2	13	9	US-09-971-980-53	Sequence 53, Appl	474	20	20.2	20	9	US-10-044-703-51	Sequence 51, Appl
402	20	20.2	13	9	US-10-015-536-19	Sequence 19, Appl	475	20	20.2	20	9	US-10-044-703-59	Sequence 59, Appl
403	20	20.2	13	9	US-10-044-703-40	Sequence 40, Appl	476	20	20.2	20	9	US-09-849-626-1835	Sequence 1835, App
404	20	20.2	13	9	US-10-215-297-14	Sequence 14, Appl	477	20	20.2	20	9	US-09-974-879-785	Sequence 285, App
405	20	20.2	13	9	US-09-352-286-13	Sequence 13, Appl	478	20	20.2	20	10	US-09-027-956-5	Sequence 5, Appl
406	20	20.2	13	9	US-09-812-485A-39	Sequence 39, Appl	479	20	20.2	20	10	US-09-731-221-64	Sequence 64, Appl
407	20	20.2	13	9	US-10-213-298-14	Sequence 14, Appl	480	20	20.2	20	10	US-09-736-076-7	Sequence 7, Appl
408	20	20.2	13	10	US-09-730-772-10	Sequence 10, Appl	481	20	20.2	20	10	US-09-735-705-243	Sequence 243, App
409	20	20.2	13	10	US-09-735-849-10	Sequence 10, Appl	482	20	20.2	20	10	US-09-735-705-377	Sequence 377, App
410	20	20.2	13	10	US-09-935-682-33	Sequence 33, Appl	483	20	20.2	20	10	US-09-841-132-262	Sequence 262, App
411	20	20.2	13	10	US-09-946-175-13	Sequence 13, Appl	484	20	20.2	20	10	US-09-308-511-14	Sequence 14, Appl
412	20	20.2	13	10	US-09-813-333-40	Sequence 40, Appl	485	20	20.2	20	10	US-09-850-716A-243	Sequence 243, App
413	20	20.2	13	10	US-09-748-114-1	Sequence 1, Appl	486	20	20.2	20	10	US-09-850-716A-377	Sequence 377, App
414	20	20.2	14	9	US-10-011-588-3	Sequence 3, Appl	487	20	20.2	20	10	US-09-813-333-51	Sequence 51, Appl
415	20	20.2	14	9	US-10-044-703-57	Sequence 57, Appl	488	20	20.2	20	10	US-09-813-333-69	Sequence 69, Appl
416	20	20.2	14	10	US-09-813-333-57	Sequence 57, Appl	489	20	20.2	20	10	US-09-897-778-243	Sequence 243, App
417	20	20.2	14	10	US-09-867-852-80	Sequence 80, Appl	490	20	20.2	20	10	US-09-897-778-377	Sequence 377, App
418	20	20.2	15	9	US-10-072-841-42	Sequence 42, Appl	491	20	20.2	21	9	US-09-974-879-410	Sequence 410, App
419	20	20.2	15	9	US-09-866-570A-29	Sequence 29, Appl	492	20	20.2	21	10	US-09-864-761-43160	Sequence 43160, A
420	20	20.2	15	9	US-10-014-485A-39	Sequence 39, Appl	493	20	20.2	21	10	US-09-864-761-43944	Sequence 43944, A
421	20	20.2	15	9	US-10-014-485A-40	Sequence 40, Appl	494	20	20.2	21	10	US-09-864-761-47384	Sequence 47384, A
422	20	20.2	15	9	US-10-153-159-40	Sequence 40, Appl	495	20	20.2	21	10	US-09-835-830-66	Sequence 66, Appl
423	20	20.2	15	9	US-09-812-485A-17	Sequence 17, Appl	496	20	20.2	21	10	US-09-835-830-66	Sequence 66, Appl
424	20	20.2	15	9	US-10-153-176-40	Sequence 40, Appl	497	20	20.2	21	10	US-09-944-849-10	Sequence 10, Appl
425	20	20.2	15	9	US-09-811-162-10	Sequence 10, Appl	498	20	20.2	22	9	US-10-038-612-115	Sequence 115, App
426	20	20.2	15	10	US-09-073-009-53	Sequence 53, Appl	499	20	20.2	22	9	US-10-038-612-115	Sequence 115, App
427	20	20.2	15	10	US-09-773-416-2	Sequence 2, Appl	500	20	20.2	22	9	US-09-815-156-8	Sequence 8, Appl
428	20	20.2	15	10	US-09-813-308-15	Sequence 15, Appl	501	20	20.2	22	10	US-09-215-652-41	Sequence 41, Appl
429	20	20.2	15	10	US-09-879-957-158	Sequence 158, App	502	20	20.2	22	10	US-09-864-761-37628	Sequence 37628, A
430	20	20.2	15	10	US-09-023-588-33	Sequence 33, App	503	20	20.2	22	10	US-09-864-761-37628	Sequence 37628, A
431	20	20.2	15	10	US-09-793-306-53	Sequence 53, Appl	504	20	20.2	22	12	US-10-066-751-102	Sequence 102, App
432	20	20.2	15	10	US-09-866-572A-29	Sequence 29, Appl	505	20	20.2	22	12	US-09-864-761-36147	Sequence 36147, A
433	20	20.2	15	12	US-10-139-841-39	Sequence 39, Appl	506	20	20.2	23	10	US-09-864-761-39030	Sequence 39030, A
434	20	20.2	15	12	US-10-139-841-40	Sequence 40, Appl	507	20	20.2	23	10	US-09-839-447A-111	Sequence 111, App
435	20	20.2	16	8	US-08-424-550B-196	Sequence 196, App	508	20	20.2	23	10	US-09-925-442-28	Sequence 28, Appl
436	20	20.2	17	9	US-09-972-137-2	Sequence 2, Appl	509	20	20.2	24	9	US-09-916-494A-18	Sequence 18, Appl
437	20	20.2	17	9	US-09-983-802-406	Sequence 406, App	510	20	20.2	24	9	US-09-999-774-26	Sequence 26, Appl
438	20	20.2	17	9	US-10-083-590-12	Sequence 12, Appl	511	20	20.2	24	9	US-09-788-308D-4	Sequence 4, Appl
439	20	20.2	17	9	US-09-925-287-1	Sequence 1, Appl	512	20	20.2	24	10	US-09-739-307-174	Sequence 174, App
440	20	20.2	17	9	US-10-087-345A-24	Sequence 24, Appl	513	20	20.2	24	10	US-09-864-761-33454	Sequence 33454, A
441	20	20.2	17	10	US-09-170-919-5	Sequence 5, Appl	514	20	20.2	24	10	US-09-864-761-34445	Sequence 34445, A
442	20	20.2	17	10	US-09-776-490-59	Sequence 59, Appl	515	20	20.2	24	10	US-09-864-761-34790	Sequence 34790, A
443	20	20.2	17	10	US-09-776-490-60	Sequence 60, Appl	516	20	20.2	24	10	US-09-864-761-35169	Sequence 35169, A
444	20	20.2	17	10	US-09-776-491-59	Sequence 59, Appl	517	20	20.2	24	10	US-09-864-761-39712	Sequence 39712, A
445	20	20.2	17	10	US-09-776-491-60	Sequence 60, Appl	518	20	20.2	24	10	US-09-864-761-45203	Sequence 45203, A
446	20	20.2	17	10	US-09-796-138-17	Sequence 17, Appl	519	20	20.2	24	10	US-09-864-761-45210	Sequence 45210, A
447	20	20.2	17	10	US-09-864-761-44102	Sequence 44102, A	520	20	20.2	24	10	US-09-864-761-46799	Sequence 46799, A
448	20	20.2	17	10	US-09-864-761-46139	Sequence 46139, A	521	20	20.2	24	10	US-09-772-719-14	Sequence 14, Appl
449	20	20.2	17	10	US-09-880-713A-12	Sequence 12, Appl	522	20	20.2	25	9	US-09-840-217-119	Sequence 119, App
450	20	20.2	17	10	US-09-880-713A-13	Sequence 13, Appl	523	20	20.2	25	9	US-10-002-344A-265	Sequence 265, App
451	20	20.2	17	10	US-09-909-903-17	Sequence 17, Appl	524	20	20.2	25	9	US-09-896-908-8	Sequence 8, Appl
452	20	20.2	17	10	US-09-969-362-15	Sequence 15, Appl	525	20	20.2	25	10	US-09-821-984-13	Sequence 13, Appl
453	20	20.2	17	10	US-09-929-986A-1	Sequence 1, Appl	526	20	20.2	25	10	US-09-864-761-38859	Sequence 38859, A
454	20	20.2	17	10	US-09-944-849-9	Sequence 9, Appl	527	20	20.2	25	10	US-09-864-761-42618	Sequence 42618, A
455	20	20.2	17	12	US-10-066-151-103	Sequence 103, App	528	20	20.2	25	10	US-09-864-761-44918	Sequence 44918, A
456	20	20.2	18	9	US-09-983-802-497	Sequence 497, App	529	20	20.2	25	10	US-09-864-761-48713	Sequence 48713, A
457	20	20.2	18	9	US-09-882-291-36	Sequence 36, Appl	530	20	20.2	25	10		

531	20	20.2	25	10	US-09-938-315-45	Sequence 45, Appl	604	19	19.2	12	9	US-09-813-153-238	Sequence 238, App
532	20	20.2	25	12	US-10-066-151-30	Sequence 30, Appl	605	19	19.2	12	10	US-09-796-254-15	Sequence 15, Appl
533	20	20.2	25	12	US-10-035-688-2	Sequence 2, Appl	606	19	19.2	12	10	US-09-832-723-40	Sequence 40, Appl
534	19.5	19.7	11	10	US-09-861-597-12	Sequence 12, Appl	607	19	19.2	13	9	US-09-949-477-15	Sequence 15, Appl
535	19.5	19.7	14	9	US-10-072-094-109	Sequence 109, App	608	19	19.2	13	9	US-09-966-955A-33	Sequence 33, Appl
536	19.5	19.7	14	9	US-10-072-094-111	Sequence 111, App	609	19	19.2	13	10	US-09-287-849-34	Sequence 34, Appl
537	19.5	19.7	15	9	US-09-848-967-14	Sequence 14, Appl	610	19	19.2	13	10	US-09-870-725-13	Sequence 13, Appl
538	19.5	19.7	17	10	US-09-823-153-6	Sequence 6, Appl	611	19	19.2	13	10	US-09-873-637-9	Sequence 9, Appl
539	19.5	19.7	17	10	US-09-902-941-1954	Sequence 1954, Ap	612	19	19.2	13	10	US-09-873-637-9	Sequence 38, Appl
540	19.5	19.7	20	9	US-09-902-941-1955	Sequence 1955, Ap	613	19	19.2	13	10	US-09-784-887B-3	Sequence 3, Appl
541	19.5	19.7	20	9	US-09-902-941-1956	Sequence 1956, Ap	614	19	19.2	14	8	US-08-873-601-13	Sequence 13, Appl
542	19.5	19.7	22	10	US-09-995-297-43	Sequence 43, Appl	615	19	19.2	14	9	US-09-954-337-7	Sequence 7, Appl
543	19.5	19.7	22	10	US-09-995-297-44	Sequence 44, Appl	616	19	19.2	14	9	US-09-966-955A-40	Sequence 40, Appl
544	19.5	19.7	22	10	US-09-995-297-45	Sequence 45, Appl	617	19	19.2	14	9	US-09-792-630-66	Sequence 66, Appl
545	19.5	19.7	24	9	US-09-983-802-661	Sequence 661, App	618	19	19.2	14	9	US-10-080-376-66	Sequence 16, Appl
546	19.5	19.7	24	9	US-09-983-802-661	Sequence 11, App	619	19	19.2	14	9	US-10-061-395-14	Sequence 14, Appl
547	19	19.2	6	9	US-09-811-162-8	Sequence 8, Appl	620	19	19.2	14	9	US-10-212-357-6	Sequence 6, Appl
548	19	19.2	7	9	US-09-851-026-19	Sequence 19, Appl	621	19	19.2	14	9	US-10-096-339-13	Sequence 13, Appl
549	19	19.2	7	9	US-09-886-429-6	Sequence 6, Appl	622	19	19.2	14	9	US-09-965-536A-46	Sequence 46, Appl
550	19	19.2	7	9	US-09-884-767A-77	Sequence 77, Appl	623	19	19.2	14	9	US-10-072-094-113	Sequence 113, App
551	19	19.2	7	9	US-09-884-767A-78	Sequence 78, Appl	624	19	19.2	14	9	US-09-791-389-161	Sequence 161, App
552	19	19.2	7	9	US-09-884-767A-135	Sequence 135, App	625	19	19.2	14	9	US-09-791-393-161	Sequence 161, App
553	19	19.2	7	10	US-09-815-330A-11	Sequence 11, Appl	626	19	19.2	14	10	US-09-157-748-20	Sequence 20, Appl
554	19	19.2	8	8	US-08-424-550B-321	Sequence 321, App	627	19	19.2	14	10	US-09-875-644-3	Sequence 8, Appl
555	19	19.2	8	8	US-10-014-485A-113	Sequence 113, App	628	19	19.2	14	10	US-09-873-637-8	Sequence 8, Appl
556	19	19.2	8	10	US-09-767-870-19	Sequence 19, Appl	629	19	19.2	14	10	US-09-781-864-1	Sequence 1, Appl
557	19	19.2	9	9	US-09-824-787B-128	Sequence 128, App	630	19	19.2	14	10	US-09-916-090-17	Sequence 17, Appl
558	19	19.2	9	9	US-09-924-400-137	Sequence 137, App	631	19	19.2	14	10	US-09-922-503-10	Sequence 10, Appl
559	19	19.2	9	9	US-09-813-718-19	Sequence 19, Appl	632	19	19.2	14	10	US-09-308-150-15	Sequence 15, Appl
560	19	19.2	9	9	US-10-143-293-5	Sequence 5, Appl	633	19	19.2	15	8	US-08-424-550B-326	Sequence 326, App
561	19	19.2	9	9	US-10-104-755-19	Sequence 19, App	634	19	19.2	15	9	US-09-826-290-149	Sequence 149, App
562	19	19.2	9	9	US-10-039-831-17	Sequence 17, Appl	635	19	19.2	15	9	US-09-826-290-159	Sequence 159, App
563	19	19.2	9	10	US-09-834-765-360	Sequence 360, App	636	19	19.2	15	9	US-09-826-290-163	Sequence 163, App
564	19	19.2	9	10	US-09-834-765-457	Sequence 457, App	637	19	19.2	15	9	US-09-175-230-11	Sequence 11, Appl
565	19	19.2	9	10	US-09-810-936-137	Sequence 137, App	638	19	19.2	15	9	US-10-010-184A-4	Sequence 4, Appl
566	19	19.2	9	10	US-09-837-723-90	Sequence 90, Appl	639	19	19.2	15	9	US-09-999-724-24	Sequence 24, Appl
567	19	19.2	9	10	US-09-428-755-137	Sequence 137, App	640	19	19.2	15	9	US-10-211-066-23	Sequence 23, Appl
568	19	19.2	9	10	US-09-780-668A-34	Sequence 34, Appl	641	19	19.2	15	9	US-09-791-389-283	Sequence 283, App
569	19	19.2	9	10	US-09-779-308-516	Sequence 516, App	642	19	19.2	15	9	US-09-791-393-293	Sequence 293, App
570	19	19.2	10	1	US-08-821-739A-99	Sequence 99, Appl	643	19	19.2	15	10	US-09-935-662-5	Sequence 5, Appl
571	19	19.2	10	8	US-08-854-825A-41	Sequence 41, Appl	644	19	19.2	15	10	US-09-873-659A-25	Sequence 25, Appl
572	19	19.2	10	9	US-09-902-432-5	Sequence 5, Appl	645	19	19.2	15	10	US-09-326-447-15	Sequence 15, Appl
573	19	19.2	10	9	US-09-902-432-8	Sequence 8, Appl	646	19	19.2	15	10	US-09-766-779A-20	Sequence 20, Appl
574	19	19.2	10	9	US-10-012-035A-29	Sequence 29, Appl	647	19	19.2	15	10	US-09-766-779A-23	Sequence 23, Appl
575	19	19.2	10	10	US-09-834-765-504	Sequence 504, App	648	19	19.2	15	10	US-09-818-364-3	Sequence 3, Appl
576	19	19.2	10	10	US-09-845-899A-16	Sequence 16, Appl	649	19	19.2	15	10	US-09-791-374-441	Sequence 441, App
577	19	19.2	10	10	US-09-779-308-58	Sequence 58, Appl	650	19	19.2	15	12	US-10-060-714-12	Sequence 12, Appl
578	19	19.2	10	10	US-09-779-308-134	Sequence 134, App	651	19	19.2	16	9	US-09-731-449-53	Sequence 53, Appl
579	19	19.2	10	10	US-09-779-308-451	Sequence 451, App	652	19	19.2	16	9	US-09-922-364A-28	Sequence 28, Appl
580	19	19.2	10	10	US-09-748-114-11	Sequence 11, App	653	19	19.2	16	9	US-09-254-590-28	Sequence 28, Appl
581	19	19.2	10	12	US-10-062-257-13	Sequence 13, Appl	654	19	19.2	16	9	US-10-115-695-28	Sequence 28, Appl
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583	19	19.2	11	9	US-09-826-290-151	Sequence 151, App	656	19	19.2	16	9	US-10-113-794A-5	Sequence 5, Appl
584	19	19.2	11	9	US-09-826-290-299	Sequence 299, App	657	19	19.2	16	9	US-09-903-412-3	Sequence 3, Appl
585	19	19.2	11	9	US-09-851-138-109	Sequence 109, App	658	19	19.2	16	9	US-10-068-564-77	Sequence 77, Appl
586	19	19.2	11	9	US-10-012-035A-28	Sequence 28, Appl	659	19	19.2	16	9	US-10-116-561-28	Sequence 28, Appl
587	19	19.2	11	9	US-10-108-195-15	Sequence 15, Appl	660	19	19.2	16	9	US-10-115-671-28	Sequence 28, Appl
588	19	19.2	11	9	US-09-811-162-9	Sequence 9, Appl	661	19	19.2	16	10	US-09-819-308-5	Sequence 5, Appl
589	19	19.2	11	9	US-10-151-568-19	Sequence 19, Appl	662	19	19.2	16	10	US-09-096-799A-3	Sequence 3, Appl
590	19	19.2	11	10	US-09-045-620-1	Sequence 1, Appl	663	19	19.2	16	10	US-09-781-804-63	Sequence 63, Appl
591	19	19.2	11	10	US-09-826-210-4	Sequence 4, Appl	664	19	19.2	16	10	US-09-883-777-15	Sequence 15, Appl
592	19	19.2	11	10	US-09-010-714-5	Sequence 5, Appl	665	19	19.2	16	10	US-09-989-903-77	Sequence 77, Appl
593	19	19.2	11	10	US-09-734-520-69	Sequence 69, Appl	666	19	19.2	16	12	US-10-051-843-2	Sequence 2, Appl
594	19	19.2	11	10	US-09-791-378-434	Sequence 434, App	667	19	19.2	17	9	US-09-966-955A-25	Sequence 25, Appl
595	19	19.2	11	11	US-09-867-852-191	Sequence 191, App	668	19	19.2	17	10	US-09-864-761-13407	Sequence 33407, A
596	19	19.2	11	12	US-10-012-034A-69	Sequence 69, Appl	669	19	19.2	17	10	US-09-864-761-16544	Sequence 36544, A
597	19	19.2	12	9	US-09-956-086-9	Sequence 9, Appl	670	19	19.2	17	10	US-09-864-761-48307	Sequence 48307, A
598	19	19.2	12	9	US-09-851-026-16	Sequence 16, Appl	671	19	19.2	17	10	US-09-326-447-17	Sequence 17, Appl
599	19	19.2	12	9	US-09-956-087-9	Sequence 9, Appl	672	19	19.2	17	10	US-09-326-447-17	Sequence 17, Appl
600	19	19.2	12	9	US-09-971-980-45	Sequence 45, Appl	673	19	19.2	18	9	US-09-805-301-92	Sequence 92, Appl
601	19	19.2	12	9	US-09-962-955C-14	Sequence 14, Appl	674	19	19.2	18	10	US-09-030-619-159	Sequence 159, App
602	19	19.2	12	9	US-09-974-879-386	Sequence 386, App	675	19	19.2	18	10	US-09-030-619-160	Sequence 160, App
603	19	19.2	12	9	US-09-325-542A-27	Sequence 27, Appl	676	19	19.2	18	10	US-09-864-761-37786	Sequence 37786, A

677	19	19.2	18	10	US-09-864-761-39324	Sequence 39324, A	750	19	19.2	23	10	US-09-739-907-1864	Sequence 184, App
678	19	19.2	18	10	US-09-864-761-46671	Sequence 46671, A	751	19	19.2	23	10	US-09-864-761-3867	Sequence 38667, A
679	19	19.2	18	10	US-09-734-520-7	Sequence 7, Appl1	752	19	19.2	23	10	US-09-864-761-42711	Sequence 42711, A
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681	19	19.2	19	9	US-10-124-903-16	Sequence 16, Appl1	754	19	19.2	23	10	US-09-785-632A-55	Sequence 55, Appl
682	19	19.2	19	9	US-09-777-328-4	Sequence 4, Appl1	755	19	19.2	23	10	US-09-785-632A-115	Sequence 115, App
683	19	19.2	19	10	US-09-864-761-36450	Sequence 36450, A	756	19	19.2	23	10	US-09-785-632A-117	Sequence 117, App
684	19	19.2	19	10	US-09-864-761-48500	Sequence 48500, A	757	19	19.2	23	10	US-09-836-865-4	Sequence 4, Appl1
685	19	19.2	19	10	US-09-735-705-388	Sequence 388, App	758	19	19.2	23	10	US-09-918-063-36	Sequence 36, Appl
686	19	19.2	19	10	US-09-850-716A-388	Sequence 388, App	759	19	19.2	23	10	US-09-928-442-27	Sequence 27, Appl
687	19	19.2	19	10	US-09-308-150-9	Sequence 9, Appl1	760	19	19.2	23	10	US-09-955-733-17	Sequence 17, Appl
688	19	19.2	19	10	US-09-897-778-388	Sequence 12, App	761	19	19.2	23	10	US-09-931-375A-79	Sequence 79, Appl
689	19	19.2	19	10	US-09-944-849-12	Sequence 37, Appl	762	19	19.2	24	9	US-09-931-375A-79	Sequence 37, Appl
690	19	19.2	20	1	US-08-785-997-37	Sequence 41, Appl	763	19	19.2	24	9	US-09-931-375A-79	Sequence 41, Appl
691	19	19.2	20	9	US-09-851-026-41	Sequence 6, Appl1	764	19	19.2	24	9	US-09-974-879-466	Sequence 365, App
692	19	19.2	20	9	US-09-878-603-6	Sequence 27, Appl	765	19	19.2	24	9	US-09-974-879-466	Sequence 466, App
693	19	19.2	20	9	US-10-029-413A-27	Sequence 25, Appl	766	19	19.2	24	10	US-09-752-724-5	Sequence 5, Appl1
694	19	19.2	20	9	US-10-032-482-25	Sequence 591, App	767	19	19.2	24	10	US-09-775-925-4	Sequence 4, Appl1
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704	19	19.2	20	10	US-09-864-761-36991	Sequence 42503, A	777	19	19.2	24	10	US-09-782-977-4	Sequence 17, Appl
705	19	19.2	20	10	US-09-864-761-40262	Sequence 42503, A	778	19	19.2	24	10	US-09-881-572A-24	Sequence 24, Appl
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707	19	19.2	20	10	US-09-864-761-43449	Sequence 8, Appl1	780	19	19.2	25	9	US-09-798-889-169	Sequence 169, App
708	19	19.2	20	10	US-09-864-761-46696	Sequence 32, Appl	781	19	19.2	25	9	US-09-813-153-275	Sequence 555, App
709	19	19.2	20	10	US-09-839-447A-9	Sequence 284, App	782	19	19.2	25	10	US-09-837-969A-22	Sequence 89, App
710	19	19.2	20	10	US-09-876-221-8	Sequence 19, Appl	783	19	19.2	25	10	US-09-864-761-35448	Sequence 22, Appl
711	19	19.2	20	10	US-09-757-417-32	Sequence 609, App	784	19	19.2	25	10	US-09-841-321A-22	Sequence 20, Appl
712	19	19.2	20	12	US-10-007-805-581	Sequence 46, Appl	785	19	19.2	25	12	US-10-071-751-70	Sequence 70, Appl
713	19	19.2	21	9	US-09-984-245-284	Sequence 4531, A	786	19	19.2	25	10	US-09-875-456A-9	Sequence 78, Appl
714	19	19.2	21	9	US-09-965-536A-19	Sequence 48960, A	787	19	19.2	25	10	US-09-873-637-4	Sequence 1, Appl1
715	19	19.2	21	9	US-09-974-879-609	Sequence 49054, A	788	19	19.2	25	10	US-08-424-550B-366	Sequence 366, App
716	19	19.2	21	9	US-09-974-879-630	Sequence 90, Appl	789	19	19.2	25	10	US-10-125-452-20	Sequence 20, Appl
717	19	19.2	21	10	US-09-853-830-42	Sequence 130, App	790	19	19.2	25	12	US-09-955-504-20	Sequence 20, Appl
718	19	19.2	21	10	US-09-853-830-90	Sequence 131, App	791	19	19.2	25	10	US-09-767-395-6	Sequence 6, Appl1
719	19	19.2	21	10	US-09-825-144-11	Sequence 10, Appl	792	19	19.2	25	10	US-09-864-761-37377	Sequence 37377, A
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722	19	19.2	21	10	US-09-864-761-48960	Sequence 49054, A	795	19	19.2	25	10	US-09-735-705-410	Sequence 410, App
723	19	19.2	21	10	US-09-864-761-49054	Sequence 90, Appl	796	19	19.2	25	10	US-09-850-716A-410	Sequence 410, App
724	19	19.2	21	10	US-09-853-830-42	Sequence 105, App	797	19	19.2	25	10	US-09-897-778-110	Sequence 18, App
725	19	19.2	21	10	US-09-853-830-90	Sequence 1, Appl	798	19	19.2	25	10	US-09-120-264-9	Sequence 9, Appl1
726	19	19.2	21	10	US-09-853-830-105	Sequence 23, Appl	799	19	19.2	25	10	US-09-995-287-46	Sequence 46, App
727	19	19.2	21	12	US-10-036-418-1	Sequence 34, Appl	800	19	19.2	25	10	US-09-995-287-46	Sequence 19, App
728	19	19.2	21	9	US-09-991-548-25	Sequence 31, Appl	801	19	19.2	25	10	US-09-185-908-37	Sequence 37, App
729	19	19.2	22	9	US-10-038-612-130	Sequence 33532, A	802	19	19.2	25	10	US-09-185-908-158	Sequence 158, App
730	19	19.2	22	9	US-09-924-400-132	Sequence 39128, A	803	19	19.2	25	12	US-09-486-734A-24	Sequence 24, App
731	19	19.2	22	9	US-09-971-980-8	Sequence 39519, A	804	19	19.2	25	9	US-09-185-908-38	Sequence 38, App
732	19	19.2	22	9	US-10-001-876-131	Sequence 42066, A	805	19	19.2	25	9	US-09-185-908-129	Sequence 129, App
733	19	19.2	22	9	US-10-140-372-14	Sequence 132, App	806	19	19.2	25	9	US-09-185-908-159	Sequence 159, App
734	19	19.2	22	9	US-09-864-761-39128	Sequence 132, App	807	19	19.2	25	9	US-09-185-908-161	Sequence 161, App
735	19	19.2	22	9	US-09-864-761-39519	Sequence 12, App	808	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
736	19	19.2	22	9	US-09-974-879-602	Sequence 592, App	809	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
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738	19	19.2	22	9	US-10-092-750-47	Sequence 592, App	811	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
739	19	19.2	22	10	US-09-780-070-34	Sequence 47, Appl	812	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
740	19	19.2	22	10	US-09-799-875-31	Sequence 34, Appl	813	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
741	19	19.2	22	10	US-09-864-761-33352	Sequence 31, Appl	814	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
742	19	19.2	22	10	US-09-864-761-33352	Sequence 31, Appl	815	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
743	19	19.2	22	10	US-09-864-761-39128	Sequence 31, Appl	816	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
744	19	19.2	22	10	US-09-864-761-39519	Sequence 31, Appl	817	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
745	19	19.2	22	10	US-09-864-761-39668	Sequence 31, Appl	818	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
746	19	19.2	22	10	US-09-864-761-42066	Sequence 31, Appl	819	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
747	19	19.2	22	10	US-09-810-936-132	Sequence 31, Appl	820	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
748	19	19.2	22	10	US-09-429-755-132	Sequence 31, Appl	821	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
749	19	19.2	22	12	US-09-747-029A-22	Sequence 31, Appl	822	19	19.2	25	10	US-09-742-315-3	Sequence 3, Appl1
					US-10-013-036-12	Sequence 12, App							
					US-09-974-879-592	Sequence 592, App							

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ALIGNMENTS

RESULT 1
US-09-808-972-11
Sequence 11, Application US/09808972
Patent No. US20020064832A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
FILE REFERENCE: 00-79
CURRENT APPLICATION NUMBER: US/09/808,972
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/132,250
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 24
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide
US-09-808-972-11

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Best local Similarity 58.3%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

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Db 4 PGMKRRGRKKT 15

RESULT 2
US-09-864-761-42868
Sequence 42868, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME- DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmlca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 42868
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.91
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US-09-864-761-42868

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; Patent No. US2002000640A1
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; APPLICANT: Ni et al.
; TITLE OF INVENTION: Uteroglobulin-Like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PM023p1
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/US00/30326
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/163,395
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-258-10

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RESULT 4

US-09-864-761-47043
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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
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; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; OTHER INFORMATION: MAP TO AC005868.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.53
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US-09-864-761-47043

Query Match 32.3%; Score 32; DB 10; Length 19;
Best Local Similarity 46.2%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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RESULT 5

US-09-864-761-43265
; Sequence 43265, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
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; PRIOR FILING DATE: 2001-01-30
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? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 43117
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 43265
? LENGTH: 20
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AL023513.1
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
? OTHER INFORMATION: EST_HUMAN HIT: F05756.1, EVALU05.00e-06
US-09-864-761-43265

```

```

? APPLICANT: Donze, David
? TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
? TITLE OF INVENTION: METHODS OF USE
? FILE REFERENCE: 05118.000802
? CURRENT APPLICATION NUMBER: US/09/955,518
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: 60/019,769
? PRIOR FILING DATE: 1996-06-14
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 14
? LENGTH: 23
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: \ No. US20020042138A1e -
? OTHER INFORMATION: synthetic construct
US-09-955-518-14

```


INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-845-667-22

Query Match 29.3%; Score 29; DB 10; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GGRGRTSS 15
111111
DB 1 GRARTSS 7

RESULT 9

US-09-867-852-95
Sequence 95, Application US/09867852
Patent No. US20020147324A1
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumitaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
CURRENT FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 09/301,085
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 95
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-867-852-95

Query Match 29.3%; Score 29; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 VPGHER 7
111111
DB 3 VPGHTR 8

RESULT 10
US-10-056-407-23
Sequence 23, Application US/10056407
Patent No. US20020165355A1
GENERAL INFORMATION:
APPLICANT: MEHENS, LYDIE
APPLICANT: LUHRMANN, REINHARD GEORGE
APPLICANT: UNION, ANN
APPLICANT: RAYACKERS, JOSEPH
TITLE OF INVENTION: METHYLATED, SMD HOMOLOGOUS PEPTIDES, REACTIVE WITH THE ANTIBODIES
TITLE OF INVENTION: SERA OF LYING BEINGS AFFECTED WITH SYSTEMIC LUPUS ERYTHEMATOSUS
FILE REFERENCE: INNS-011-1
CURRENT APPLICATION NUMBER: US/10/056,407

CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: US 09/297,981
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-10-056-407-23

Query Match 29.3%; Score 29; DB 9; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 GHERMGGR 12
111111
DB 7 GNGRGGR 15

RESULT 11

US-09-847-519A-3
Sequence 3, Application US/09847519A
Patent No. US20020102693A1
GENERAL INFORMATION:
APPLICANT: Lucche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125,422
CURRENT APPLICATION NUMBER: US/09/847,519A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DSP-14 active site
US-09-847-519A-3

Query Match 29.3%; Score 29; DB 10; Length 19;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 5 HERMGRTSKELA 19
111111
DB 2 HCVMGRRSATLVLA 16

RESULT 12
US-09-864-761-46793
Sequence 46793, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeonica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46793
LENGTH: 23
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000177.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
US-09-664-761-46793

Query Match
Best Local Similarity 29.3%; Score 29; DB 10; Length 23;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VPGHRMG 9
Db 13 IPAHYRLG 20

RESULT 13
US-09-664-761-38863
Sequence 38863, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: A60163-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38863
LENGTH: 25
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL035681.13
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EST_HUMAN HIT: BF346206.1, EVALUATE 5.00e-06
US-09-664-761-38863

Query Match
Best Local Similarity 29.3%; Score 29; DB 10; Length 25;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MGRGRTS 14
Db 17 LGGGRTS 23

RESULT 14
US-08-424-550B-242
Sequence 242, Application US/08424550B
Patent No. US20020119447A1
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:

TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-845-667-35

Query Match 27.3%; Score 27; DB 10; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GGRPTSS 15
DB 1 GGRPTSS 7

RESULT 18
US-10-108-795-26
Sequence 26, Application US/10108795
Publication No. US2003003363A1
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian A
TITLE OF INVENTION: Calcium Regulated Kinase
FILE REFERENCE: 30110
CURRENT APPLICATION NUMBER: US/10/108,795
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 09/133,062
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: GB 9717089, 8
PRIOR FILING DATE: 1997-08-12
PRIOR APPLICATION NUMBER: GB 9717499, 9
PRIOR FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
-10-108-795-26

Query Match 27.3%; Score 27; DB 9; Length 11;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GGRPTSS 15
DB 1 GGRPTSS 7

RESULT 19
US-09-845-667-1
Sequence 1, Application US/09845667
Patent No. US20020065221A1
GENERAL INFORMATION:
APPLICANT: Cohen, Philip
Alessi, Dario
Cross, Datten
TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
FOR AGENTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Braham & Rogalsky, LLP
STREET: P. O. Box 352
CITY: Canandaigua

STATE: New York
COUNTRY: USA
ZIP: 14424-0352
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998
APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Braham, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002,00041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-845-667-1

Query Match 27.3%; Score 27; DB 10; Length 11;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GGRPTSS 15
DB 1 GGRPTSS 7

RESULT 20
US-09-966-782A-39
Sequence 39, Application US/09966782A
Publication No. US20030022183A1
GENERAL INFORMATION:
APPLICANT: Battaglini, P.
Feder, J. N.
APPLICANT: Mintier, G.
APPLICANT: Ramanathan, C. S.
APPLICANT: Westphal, R.
APPLICANT: Hawken, D. R.
APPLICANT: Cacace, A.
APPLICANT: Barber, L.
APPLICANT: Kornacker, M. G.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRMY7,
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRMY7,
FILE REFERENCE: D0044NP
CURRENT APPLICATION NUMBER: US/09/966,782A
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,731
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/268,580
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/315,423

PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-966-782A-39

Query Match 27.3%; Score 27; DB 9; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 GGRGRTSSKEL 18
DB 2 GKGRTERAEI 11

RESULT 21
US-09-867-852-73
Sequence 73, Application US/09867852
Patent No. US2002014732A1
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mandinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
FILE REFERENCE: 00786/254002
CURRENT APPLICATION NUMBER: US/09/867,852
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 73
LENGTH: 15
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-867-852-73

Query Match 27.3%; Score 27; DB 10; Length 15;
Best Local Similarity 41.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GHERMGRTSS 15
DB 3 GHRUGENWSSS 14

RESULT 22
US-09-987-456-13
Sequence 13, Application US/09987456
Patent No. US20020123057A1
GENERAL INFORMATION:
APPLICANT: University of Rochester
APPLICANT: Zauderer, Maurice
APPLICANT: Ernest S. Smith
TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
Immunoglobulin Molecules In Eukaryotic Cells
FILE REFERENCE: 1821.0070004

CURRENT APPLICATION NUMBER: US/09/987,456
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/271,424
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/262,067
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/298,087
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/249,268
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: linker peptide
US-09-987-456-13

Query Match 27.3%; Score 27; DB 10; Length 16;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GRTSSKELA 19
DB 3 GSVSSELA 11

RESULT 23
US-09-955-732-18
Sequence 18, Application US/09955732
Patent No. US20020182203A1
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.433
CURRENT APPLICATION NUMBER: US/09/955,732
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
US-09-955-732-18

Query Match 27.3%; Score 27; DB 9; Length 22;
Best Local Similarity 40.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 5 HERMGRTSSKELA 19
DB 4 HCKMGVSRAATVLA 18

RESULT 24
US-09-845-667-45
Sequence 45, Application US/09845667
Patent No. US20020065221A1
GENERAL INFORMATION:
APPLICANT: Cohen, Phillip
APPLICANT: Alessi, Dario
APPLICANT: Cross, Darren
TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
FOR AGENTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bramer & Rogalskyj, LLP
STREET: P.O. Box 352
CITY: Canandaigua
STATE: New York

COUNTRY: USA
ZIP: 14424-0352
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998
APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Braham, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002,00041
TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-845-667-45

Query Match 26.3%; Score 26; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 RGRSSK 16
Db 1 RPRSSK 7

ULF 25
us-10-012-756-19
Sequence 19, Application US/10012756
Patent No. US20020164355A1
GENERAL INFORMATION:
APPLICANT: John B. Harley and Judith A. James
TITLE OF INVENTION: Diagnostics And Therapy Of Epstein-Barr
Virus In Autoimmune Disorders
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30306-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/012,756
FILING DATE: 24-Oct-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,296
FILING DATE: 13-JAN-1997
APPLICATION NUMBER: 60/019,053
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: 08/160,604
FILING DATE: 30-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 19
US-10-012-756-19

Query Match 26.3%; Score 26; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 RMRGR 12
Db 7 RGRGR 12

Search completed: March 14, 2003, 16:10:58
Job time : 34 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:03:12 ; Search time 10 Seconds
(without alignments)
78.805 Million cell updates/sec

Title: US-09-674-913a-1
Perfect score: 99
Sequence: 1 NVPCHERMGRGRTSSKELA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1520

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	30	30.3	15	1	UC08_MAIZE
2	30	30.3	23	1	CP23_SPOER
3	30	30.3	23	1	PAP1_SPOEX
4	30	30.3	23	1	PAP2_SPOEX
5	30	30.3	23	1	PAP3_SPOEX
6	29	29.3	23	1	PAP1_HELVY
7	29	29.3	23	1	PAP2_HELVY
8	27	27.3	14	1	ADF_TENMO
9	25	25.3	24	1	DNM1_STRAG
10	24	24.2	15	1	DCNM_PSECH
11	24	24.2	25	1	DNM1_MYCCA
12	23	23.2	20	1	KORA_METTM
13	22	22.2	12	1	H2AX_ONCMY
14	22	22.2	22	1	TIH1_SPTOL
15	22	22.2	25	1	G3P2_JACOR
16	22	22.2	25	1	METE_GANAL
17	21	21.2	18	1	IBP4_PIG
18	21	21.2	16	1	MLB_SCYCA
19	21	21.2	20	1	PORC_METTM
20	21	21.2	25	1	NEUR_RANTE
21	20.5	20.7	24	1	PGO_XENLA
22	20	20.2	7	1	CHOX_PIG
23	20	20.2	17	1	PNOC_PIG
24	20	20.2	17	1	PKK5_PERAM
25	20	20.2	19	1	TX3_PHONI
26	20	20.2	20	1	AROQ_AMEME
27	20	20.2	20	1	LEC1_ARTIN
28	20	20.2	20	1	SAMP_PLEPL
29	20	20.2	21	1	LEC2_ARTIN
30	20	20.2	25	1	GBP_APAKA
31	19	19.2	15	1	ONC1_ONCMY
32	19	19.2	16	1	HBD_CLOPA
33	19	19.2	17	1	APTD_BOMPA

34	19	19.2	17	1	RS13_PARDE
35	19	19.2	20	1	PNV2_PHONI
36	19	19.2	23	1	CH60_THIFE
37	19	19.2	25	1	FRHB_METBA
38	19	19.2	25	1	GUNI_CLOJO
39	18	18.2	9	1	FIIB_PAPAN
40	18	18.2	10	1	PCIR_DIAAB
41	18	18.2	10	1	PAP1_PARMA
42	18	18.2	11	1	MLG_THERS
43	18	18.2	14	1	RS19_PROAP
44	18	18.2	20	1	CUDP_VERCH
45	18	18.2	20	1	DETS_RAT
46	18	18.2	20	1	RIPX_CUCPE
47	18	18.2	21	1	GYRA_STRSH
48	18	18.2	23	1	AU41_LITRA
49	18	18.2	23	1	AU44_LITRA
50	18	18.2	23	1	PAP1_MANSE
51	18	18.2	25	1	CXOB_CONCT
52	17.5	17.7	12	1	RS19_ELYEP
53	17	17.2	8	1	ACI_THUAL
54	17	17.2	8	1	FUSS_FUSSO
55	17	17.2	8	1	UPAI_HUMAN
56	17	17.2	8	1	VLG6_HSV2B
57	17	17.2	9	1	FAR5_CALVO
58	17	17.2	9	1	NSK1_SARBU
59	17	17.2	10	1	LSK2_LEUMA
60	17	17.2	11	1	LSK1_LEUMA
61	17	17.2	11	1	LSKP_PERAM
62	17	17.2	12	1	LOSK_LOCMI
63	17	17.2	13	1	MLA_ANOCA
64	17	17.2	13	1	MLA_CAMDR
65	17	17.2	14	1	NSK2_SARBU
66	17	17.2	14	1	PKK6_SCHGR
67	17	17.2	14	1	TKN1_SCHGR
68	17	17.2	15	1	METK_MAIZE
69	17	17.2	16	1	MMPX_SOLTU
70	17	17.2	16	1	RIPK_TRIKI
71	17	17.2	17	1	PATS_ANASP
72	17	17.2	18	1	MLB_HORSE
73	17	17.2	19	1	FRHG_METBA
74	17	17.2	19	1	MEFH_TRIMR
75	17	17.2	19	1	TRP3_LEUMA
76	17	17.2	20	1	COXF_ONCMY
77	17	17.2	20	1	FRHA_METBA
78	17	17.2	20	1	MEF_PIG
79	17	17.2	20	1	PSAF_MAIZE
80	17	17.2	20	1	PSAF_PEA
81	17	17.2	20	1	RECX_AZOVI
82	17	17.2	21	1	DIAG_AMEME
83	17	17.2	22	1	TX1_HETFU
84	17	17.2	23	1	NEU1_LITCE
85	17	17.2	23	1	TX2_HETFU
86	17	17.2	23	1	TYPH_LACCA
87	17	17.2	24	1	BOMN_BOMVA
88	17	17.2	25	1	BLP4_BOMOR
89	17	17.2	25	1	BOTR_BORJA
90	17	17.2	25	1	H11_WHEAT
91	17	17.2	25	1	RL36_MYCCA
92	17	17.2	25	1	RS19_ACHLA
93	17	17.2	25	1	Y194_ARCFU
94	16.5	16.7	23	1	CHIB_PEA
95	16.5	16.7	24	1	KAD_BACLI
96	16	16.2	8	1	ICK2_LEUMA
97	16	16.2	9	1	YBFR_AZOVI
98	16	16.2	10	1	BPP8_BORIN
99	16	16.2	10	1	COXO_RAT
100	16	16.2	10	1	TPIS_NICPL
101	16	16.2	12	1	RR16_GINBI
102	16	16.2	12	1	RS19_TOBBP
103	16	16.2	12	1	UH03_RAT
104	16	16.2	13	1	BRP1_BORJA
105	16	16.2	13	1	IDHA_CANFA
106	16	16.2	14	1	NEJ2_FASHE

P72180	paracoccus
O91wr5	phoenicia
P29134	thiobacilli
P80490	methanosarc
P17877	clostridium
P19344	papio anubi
P1179	diaprepes a
P1863	parachirrus
P41989	theromyzon
O44160	prunus arme
P80406	verticilliu
P07448	rattus norv
P80750	cucurbita p
P50071	streptomyce
P82397	litorea aur
P82400	litorea ran
P30253	manduca sex
P58918	conus calus
O47881	elm yellows
P18691	thunnus alb
P81010	fusarium so
P30087	homo sapien
P81780	herpes simp
P41860	calliphora
P41492	sarcophaga
P09039	leucophaea
P04428	leucophaea
P36885	periplaneta
P47733	locusta mig
P41589	anolis caro
P01198	camelus dro
P41493	sarcophaga
P82693	periplaneta
P82470	schistocerc
P80616	zea mays (m
P80501	solanum tub
P16093	trichosanthe
O52748	anabena sp
P01202	equus cabal
P80491	methanosarc
P81530	trichuris m
P81735	leucophaea
P80329	oncohychnu
P80493	methanosarc
P80928	sus scrofa
P13119	zea mays (m
P20113	pisum sativ
P37853	azotobacter
P80414	amycolalops
P82850	heterometru
P81872	litorea cae
P82851	heterometru
P15663	lactobacilli
P01505	bombina var
P29005	bombina ori
P22028	bothrops ja
P15871	triticum ae
O48972	mycoplasma
P29224	achetepiasm
O30045	archaeoglob
P21227	pisum sativ
P25140	bacillius ii
P21141	leucophaea
P25865	azotobacter
P30465	azotobacter
P80432	bothrops in
P81918	rattus norv
P36207	nicotiana p
O56213	gingko bilo
P56572	tomato big
P01070	bothrops ja
P54836	canis famill
P80526	fasciola he

107	16	16.2	14	1	RS19_PWPBP	Q52093	pigeon pea	180	15	15.2	20	1	SB60_MAIZE	P82868	zea mays (m
108	16	16.2	14	1	SAP2_ARBPV	P11760	arabacia pun	181	15	15.2	21	1	NDK_CANAL	O9u06	candida alb
109	16	16.2	15	1	ODP3_SOLTU	P81420	solanum tub	182	15	15.2	21	1	NR1A_ACTIP	P3306	acinetobact
110	16	16.2	16	1	MLB_SOTAC	P01207	squalus aca	183	15	15.2	21	1	PEDE_HYDAT	P80577	hydra atten
111	16	16.2	17	1	AU31_LITRA	P82394	litorea ran	184	15	15.2	21	1	TKNC_CARAU	P23421	carassius a
112	16	16.2	17	1	AU32_LITRA	P82395	litorea ran	185	15	15.2	21	1	TRYE_PROAT	P35051	protipterus
113	16	16.2	17	1	AU33_LITRA	P82396	litorea ran	186	15	15.2	22	1	DP20_CAEBR	P51558	caenorhabdi
114	16	16.2	17	1	RM35_YEAST	P36530	saccharomyc	187	15	15.2	23	1	COX2_ONCMY	P80333	oncorhynch
115	16	16.2	17	1	TL09_SPIOL	P82671	spinnacia ol	188	15	15.2	23	1	NITP_ANASL	P33177	anabaena sp
116	16	16.2	17	1	VESP_VESMC	P57672	vespula mac	189	15	15.2	23	1	PAP2_MANSE	P30574	manduca sex
117	16	16.2	18	1	GOME_ACAGO	P82358	acanthoscur	190	15	15.2	23	1	RL18_HALVO	P50563	halobacteri
118	16	16.2	19	1	FIBB_CERNI	P14447	cervus nipp	191	15	15.2	23	1	VG22_BPT2	P21596	bacterioph
119	16	16.2	19	1	FIBB_HORSE	P14471	equus cabal	192	15	15.2	24	1	12KD_MYCSM	P80438	mycobacteri
120	16	16.2	20	1	CISY_STRHY	P20903	streptomyce	193	15	15.2	24	1	COX3_SHEEP	O9r230	ovis aries
121	16	16.2	20	1	FIBR_PACLE	P81070	pacifastacu	194	15	15.2	24	1	CRTC_CANFA	P28490	canis famli
122	16	16.2	20	1	FRR3_LITIN	P56249	litorea inf	195	15	15.2	24	1	FEDG_AMEYE	P80707	ameciolapops
123	16	16.2	20	1	MCRG_METTE	P22950	methanosarc	196	15	15.2	24	1	IR31_HAEIN	P35756	haemophilus
124	16	16.2	20	1	PURK_RROSH	O53121	rhodobacter	197	15	15.2	24	1	PSBR_WHEAT	P12358	triticum ae
125	16	16.2	20	1	SCB1_CANFA	P99507	canis famli	198	15	15.2	25	1	AMP3_MELGA	P80393	melagrifis g
126	16	16.2	21	1	ACE_BOVIN	P21332	corynebacte	199	15	15.2	25	1	H2B1_ECHES	P13381	echinus esc
127	16	16.2	22	1	LPRM_CORDI	P12820	bos taurus	200	15	15.2	25	1	LPCP_YEAST	P08521	saccharomyc
128	16	16.2	22	1	LANM_STRMU	P80666	streptococc	201	15	15.2	25	1	RL41_ARATH	P35015	arabidopsi
129	16	16.2	22	1	NUEM_SOLTU	P80765	solanum tub	202	15	15.2	25	1	RL41_HUMAN	P28751	homo sapien
130	16	16.2	22	1	NUO7_SOLTU	P80730	solanum tub	203	15	15.2	25	1	RL41_QUESU	O82713	quercus sub
131	16	16.2	22	1	PSP2_PHYPA	P80661	physcomlitre	204	15	14.6	12	1	UKA2_HUMAN	P31144	homo sapien
132	16	16.2	23	1	PS3_PSPBP	P81390	pseudis par	205	14.6	14.6	22	1	FUC1_RAT	P80347	rattus norv
133	16	16.2	23	1	VG22_BPT6	P21597	bacterioph	206	14	14.1	7	1	DCML_PSECH	P19916	pseudomonas
134	16	16.2	24	1	DHAG_COMTE	P80705	comamonas t	207	14	14.1	7	1	UN06_PINPS	P81675	pinus pinas
135	16	16.2	24	1	FIRB_CANFA	P12800	canis famli	208	14	14.1	8	1	PPK3_PERAM	P82618	periplaneta
136	16	16.2	24	1	HPPA_RABIT	P13571	oryctolagus	209	14	14.1	9	1	LITO_LITRAU	P08945	litorea aur
137	16	16.2	24	1	RS13_THETU	P80377	thermus the	210	14	14.1	9	1	LITR_PHYRO	P08946	phyllomedus
138	16	16.2	24	1	RS19_PHYS2	O60696	phytoplasm	211	14	14.1	10	1	GLEM_HUMAN	P02728	homo sapien
139	16	16.2	25	1	COX1_PARVE	O00502	paracoccus	212	14	14.1	10	1	GON2_CHEPR	P80678	cheilyosoma
140	16	16.2	25	1	COX6_NEUCR	O01359	neurospora	213	14	14.1	10	1	GON3_ONCKE	P20367	oncorhynch
141	16	16.2	25	1	CXOB_CONMA	P05485	conus magus	214	14	14.1	10	1	GONL_SQUAC	P27429	squalus aca
142	16	16.2	25	1	RL41_SOYEN	O49324	glycine max	215	14	14.1	10	1	GRP_RANRI	P23260	rana ridibu
143	15.5	15.7	18	1	CPAX_BOVIN	P22779	bos taurus	216	14	14.1	10	1	SPI_HALRO	O10997	halocynthia
144	15.5	15.7	22	1	FUC2_RAT	P80348	rattus norv	217	14	14.1	10	1	UPA5_HUMAN	P30091	homo sapien
145	15.5	15.7	25	1	CP12_SOLTU	P24744	solanum tub	218	14	14.1	11	1	COR2_PERAM	P1496	periplaneta
146	15	15.2	3	1	GRWM_HUMAN	P01157	homo sapien	219	14	14.1	11	1	MORL_HUMAN	P01163	homo sapien
147	15	15.2	10	1	COXK_ONCMY	P80332	oncorhynch	220	14	14.1	11	1	RANC_RANPI	P08951	rana pipien
148	15	15.2	10	1	COXO_THUOB	P80982	thunnus obe	221	14	14.1	12	1	OPS3_DROVI	P17645	drosophila
149	15	15.2	11	1	TKND_RANRI	P29207	rana ridibu	222	14	14.1	12	1	SOIS_BACSU	P80863	baetisflus su
150	15	15.2	11	1	TKND_RANCA	P22691	rana catesb	223	14	14.1	12	1	UR2_POLSP	P81022	polyodon sp
151	15	15.2	12	1	RS19_CLEPE	O46490	clever yell	224	14	14.1	13	1	BOML_PSEGU	P40297	pseudophryn
152	15	15.2	12	1	TA10_TREME	P01371	tremella me	225	14	14.1	13	1	ITB5_BOVIN	P80741	bos taurus
153	15	15.2	12	1	VI4K_MSSV	P82006	white spot	226	14	14.1	13	1	SAZ8_ONCMY	P82238	oncorhynch
154	15	15.2	13	1	ORCK_ORCLI	P37086	orconectes	227	14	14.1	13	1	SAZ8_ONCMY	P82239	oncorhynch
155	15	15.2	14	1	LPW_CITFR	P03056	citrobacter	228	14	14.1	14	1	ALYT_ALYOB	P08944	alytes obst
156	15	15.2	14	1	LPW_ECOLI	P03054	escherichia	229	14	14.1	14	1	FIBR_HORSE	P14452	equus cabal
157	15	15.2	14	1	LPW_SALTU	P03054	salmonella	230	14	14.1	14	1	MCRZ_METTM	P58676	methanobact
158	15	15.2	14	1	RS19_CLOPP	O46228	clover prol	231	14	14.1	14	1	MY14_EISFO	P46579	eisenia foe
159	15	15.2	14	1	RS19_LOMBP	O48878	loofah witc	232	14	14.1	14	1	MY14_PHEVI	P46880	pheretima v
160	15	15.2	15	1	CYSK_CLOPA	P81340	clostridium	233	14	14.1	14	1	TAT1_HV1W2	P12509	human immun
161	15	15.2	15	1	EF1A_MTCCK	P81266	microplitis	234	14	14.1	14	1	TAT1_HV1Z8	P12511	human immun
162	15	15.2	15	1	MCA2_RHOOP	P56870	rhodococcus	235	14	14.1	14	1	UN46_CLOPA	P81362	clostridium
163	15	15.2	15	1	SALI_ONCMY	P81369	oncorhynch	236	14	14.1	15	1	ALB2_TRASC	P81189	tracheux s
164	15	15.2	15	1	TERM_BPM2	P19897	bacterioph	237	14	14.1	15	1	ESTR_MANSE	P19875	manduca sex
165	15	15.2	16	1	DBH3_RHILE	P80605	rhizobium l	238	14	14.1	15	1	EGF1_CANFA	P18651	canis famli
166	15	15.2	16	1	PIRA_MUSVI	P14458	musclela vis	239	14	14.1	15	1	MAOX_CHICK	O92060	gallus gall
167	15	15.2	16	1	PPAC_BACME	P56948	baetisflus me	240	14	14.1	16	1	FIBR_ODOHE	P14459	odocoileus
168	15	15.2	17	1	B29K_PORGI	P81784	porphyromon	241	14	14.1	16	1	FORL_MYRGU	P81438	myrmecia gu
169	15	15.2	17	1	BOLA_MEGPE	P07495	megabombus	242	14	14.1	16	1	SALI_ONCMY	P82240	oncorhynch
170	15	15.2	18	1	NPA_BOVIN	P15506	bos taurus	243	14	14.1	17	1	EFG_THEAO	O01697	thermus aqu
171	15	15.2	18	1	PH1_PERAM	P82694	periplaneta	244	14	14.1	17	1	PH4_PERAM	P82697	periplaneta
172	15	15.2	18	1	RL24_PROVU	P20032	procteus vul	245	14	14.1	17	1	PSBL_STYNU	P12241	synecococc
173	15	15.2	19	1	PAZS_HUMAN	P24606	homo sapien	246	14	14.1	17	1	RANR_RANRU	P08952	rana rugosa
174	15	15.2	19	1	RS19_SPEIC	O31159	spiroplasma	247	14	14.1	17	1	UP36_UPEMT	P0263	uperoleia m
175	15	15.2	20	1	CAT4_FASHE	P80528	fasciola he	248	14	14.1	18	1	AGI_EUPMA	P33889	euphorbia m
176	15	15.2	20	1	DNAK_CLOPA	P81341	clostridium	249	14	14.1	19	1	ADC_CLOPA	P81336	clostridium
177	15	15.2	20	1	DNAK_THIEF	P29133	thiobacillu	250	14	14.1	19	1	BRKM_BOMAX	P83055	bombina max
178	15	15.2	20	1	OXLA_CEOAT	P56742	crotalus at	251	14	14.1	19	1	FIBR_CEREL	P14446	cervus elap
179	15	15.2	20	1	PSBW_WHEAT	P55967	triticum ae	252	14	14.1	19	1	FIBR_SHEEP	P14451	ovis aries

253	14	14.1	19	1	LCRP_PETMA	010996	petromyzon	326	13	13.1	10	1	GONI_CLUPA	P81749	clupea pall
254	14	14.1	19	1	PCG7_PACGO	P82420	pachycondyl	327	13	13.1	10	1	GONI_PETMA	P04378	petromyzon
255	14	14.1	20	1	ALAT_PIG	P13191	sus scrofa	328	13	13.1	10	1	GONI2_CHICK	P30743	gallus gall
256	14	14.1	20	1	COXB_THUOB	P80974	thunnus obe	329	13	13.1	10	1	GONI3_PETMA	P30948	petromyzon
257	14	14.1	20	1	EFVU_MYCSI	P81407	mycoplasma	330	13	13.1	10	1	HTE_NAUCI	P10939	nauphoeta c
258	14	14.1	20	1	FLAW_AZOVI	P52964	azotobacter	331	13	13.1	10	1	HTE_TABAT	P14596	tabanus atr
259	14	14.1	20	1	HELT_HRLHO	P46693	heloderma h	332	13	13.1	10	1	PNEU_HUMAN	P22103	homo sapien
260	14	14.1	20	1	ITRA_ALBUO	P24925	albizzia ju	333	13	13.1	10	1	PNEU_RAT	P21996	rattus norv
261	14	14.1	20	1	LEC3_ARTIN	P18673	artocarpus	334	13	13.1	10	1	SLAP_BACTG	P49325	bacillus th
262	14	14.1	20	1	PSAL_SYNVU	P25337	synecchococ	335	13	13.1	10	1	VEG6_BACSU	P80699	bacillus su
263	14	14.1	20	1	SB18_MAIZE	P82667	zea mays (m	336	13	13.1	11	1	ANCT_CRIGE	P09037	crinia geor
264	14	14.1	20	1	VSP1_AGRBI	P33588	agkistrodon	337	13	13.1	11	1	BRP_AGRHP	P04562	agkistrodon
265	14	14.1	20	1	YOH_KLEAE	P56506	klebsiella	338	13	13.1	11	1	BRK_MEGFL	P12797	megascollia
266	14	14.1	21	1	FIIB_BUBBU	P14467	bubalus bub	339	13	13.1	11	1	COXA_CANFA	P99501	canis famli
267	14	14.1	21	1	REV_HV2D2	P15830	human immun	340	13	13.1	11	1	LAD1_ONCMY	P81018	oncorhynch
268	14	14.1	21	1	SYA_RAT	P50475	rattus norv	341	13	13.1	11	1	LFW_THETH	P05624	thermus the
269	14	14.1	21	1	YD90_HAEIN	P45194	haemophilus	342	13	13.1	11	1	TKNA_ONCMY	P28499	oncorhynch
270	14	14.1	22	1	ANFC_CHICK	P21805	gallus gall	343	13	13.1	11	1	TKNA_SCYCA	P41333	scyllorhinu
271	14	14.1	22	1	CR34_LITCE	P56241	littoria cae	344	13	13.1	12	1	PORD_METTM	P80903	methanobact
272	14	14.1	22	1	RL41_METJA	P54025	methanococ	345	13	13.1	13	1	BRK_PARDI	P42717	parapolybia
273	14	14.1	23	1	AL15_HORSE	P82616	equus cabal	346	13	13.1	13	1	CXA2_CONGE	P01520	conus geogr
274	14	14.1	23	1	AU42_LITRA	P82398	littoria ran	347	13	13.1	13	1	CXA4_CONST	P28878	conus stria
275	14	14.1	23	1	AU43_LITAU	P82399	littoria aur	348	13	13.1	13	1	FIBA_CAVPO	P14445	cavia porce
276	14	14.1	23	1	GRP_ONCMY	O9ps30	oncorhynch	349	13	13.1	13	1	TEML_RANTE	P56917	rana tempor
277	14	14.1	23	1	MDH_THREAU	P33163	thermoleoph	350	13	13.1	13	1	UN12_CLOPA	P81353	clostridium
278	14	14.1	23	1	RT21_BOVIN	P82920	bos taurus	351	13	13.1	13	1	CXA1_CONCN	P56973	conus conso
279	14	14.1	24	1	TL17_SPIOLO	P81778	splachia ol	352	13	13.1	14	1	CXA1_CONMA	P01521	conus magus
280	14	14.1	24	1	CCAA_STRTTI	P80436	streptomyce	353	13	13.1	14	1	FIIB_MANLE	P14474	mandrillus
281	14	14.1	24	1	CT31_LITCI	P81851	littoria cit	354	13	13.1	14	1	IFP2_RAT	P81795	rattus norv
282	14	14.1	24	1	DMS6_PHYBI	P81490	phyllomedus	355	13	13.1	14	1	UC18_MAIZE	P80624	zea mays (m
283	14	14.1	24	1	IMPI_GALME	P82176	galleria me	356	13	13.1	14	1	UN07_CLOPA	P81352	clostridium
284	14	14.1	24	1	PCL2_PACGO	P82421	pachycondyl	357	13	13.1	14	1	COXJ_THUOB	P80979	thunnus obe
285	14	14.1	24	1	PCL2_PACGO	P82422	pachycondyl	358	13	13.1	15	1	CXA1_THUOB	P58624	conus betul
286	14	14.1	24	1	PSAH_CUCISA	P42050	cucumis sat	359	13	13.1	15	1	FIBA_ANAPL	P12801	anus platyr
287	14	14.1	24	1	RELI_ECOLI	P56980	escherichia	360	13	13.1	15	1	GLN2_PINPS	P81107	pinus pinas
288	14	14.1	24	1	REI2_ECOLI	O9wtat7	escherichia	361	13	13.1	15	1	KLOM_LUMTE	P11918	lunibricus t
289	14	14.1	24	1	TX6B_PHYSE	P58912	phyllodiscu	362	13	13.1	15	1	PH2_PBRAM	P82695	microplaneta
290	14	14.1	24	1	VFB_BPD10	P13771	bacterioph	363	13	13.1	15	1	PLAS_MICAE	P10625	microcystis
291	14	14.1	24	1	Y3KD_NEUCR	P22702	neurospora	364	13	13.1	15	1	TA1_TREBR	P34070	tremella br
292	14	14.1	25	1	ACP_ACICPA	P80916	actinetobact	365	13	13.1	15	1	UC16_MAIZE	P80622	zea mays (m
293	14	14.1	25	1	COXO_ONCMY	P80937	alcaligenes	366	13	13.1	15	1	UC19_MAIZE	P80625	zea mays (m
294	14	14.1	25	1	CR22_LITGI	P56234	littoria gil	368	13	13.1	15	1	UN01_PINPS	P81106	pinus pinas
295	14	14.1	25	1	CR25_LITGI	P56237	littoria gil	369	13	13.1	15	1	UN04_PINPS	P81673	pinus pinas
296	14	14.1	25	1	GLMK_PREBR	P82680	prevotella	370	13	13.1	15	1	AL11_CALVO	P41839	calliphora
297	14	14.1	25	1	IPYR_PSEAN	P09472	scyllorhinu	371	13	13.1	16	1	FENR_STRGR	P24134	streptomyce
298	14	14.1	25	1	GRP_SCYCA	P80888	pseudonabae	372	13	13.1	16	1	FIBA_MELME	P14456	meles meles
299	14	14.1	25	1	NEUU_CHICK	P34963	gallus gall	373	13	13.1	16	1	FIIB_RABIT	P14651	oryctolagus
300	14	14.1	25	1	RS11_THETH	P80376	thermus the	374	13	13.1	16	1	PA21_TRIST	P82892	trimeresuru
301	14	14.1	25	1	RT06_BOVIN	P82931	bos taurus	375	13	13.1	16	1	UVSX_BPT6	O06728	bacterioph
302	14	14.1	25	1	VCG_BP64	P03632	bacterioph	376	13	13.1	17	1	AL1S_MYCPH	P81528	mycobacteri
303	14	14.1	17	1	NEF_HV1J3	P12480	human immun	377	13	13.1	17	1	BOLS_MEGPE	P07496	megabombus
304	13.5	13.6	20	1	LEC2_MACPO	P18676	macclura pom	378	13	13.1	17	1	PH3_PBRAM	P82696	microplaneta
305	13.5	13.6	7	1	FAR2_ASCSU	P18990	ascaris su	379	13	13.1	18	1	A2M_OCTYU	P30800	ocotopus vul
306	13	13.1	7	1	UF03_MOUSE	P38641	mus musculu	380	13	13.1	18	1	SODM_MYCHA	P80582	mycobacteri
307	13	13.1	7	1	WMA3_ACHPU	P55921	echatina fu	381	13	13.1	18	1	YAA5_RHOPA	O02005	rhodopseudo
308	13	13.1	8	1	AAH_TABAT	P14595	tabanus atr	382	13	13.1	18	1	YPE4_LACLC	P42022	lactococcus
309	13	13.1	8	1	ICK5_LEUMA	P19987	leucophaea	383	13	13.1	19	1	FIIB_BOBBU	P14442	bubalus bub
310	13	13.1	8	1	LPMS_STEAP	P23211	staphylococ	384	13	13.1	19	1	HBB2_UR0HA	P18992	urumastyx h
311	13	13.1	8	1	RPCH_PANNO	P08939	pandalus bo	385	13	13.1	19	1	H170_RAT	P21794	rattus norv
312	13	13.1	8	1	UF06_MOUSE	P38644	mus musculu	386	13	13.1	19	1	HMD_METMO	P32441	m coenzyme
313	13	13.1	8	1	UFPA_HUMAN	P30096	homo sapien	387	13	13.1	19	1	TP1S_CLOPA	P81348	clostridium
314	13	13.1	9	1	FIAB_CALSI	P38495	callicnectes	388	13	13.1	19	1	UP25_UPEIN	P82031	uperoleia l
315	13	13.1	9	1	FIIB_MACFU	P19345	macaca fusc	389	13	13.1	19	1	UP27_UPEMJ	P82039	uperoleia m
316	13	13.1	9	1	FIIB_PAPHA	P19343	papio hamad	390	13	13.1	19	1	UP28_UPEMJ	P82040	uperoleia m
317	13	13.1	9	1	SAMP_MUSCA	P19095	muscielus ca	391	13	13.1	20	1	ABP_PIG	O9trc7	sus scrofa
318	13	13.1	9	1	UTAH_HUMAN	P31934	homo sapien	392	13	13.1	20	1	BULB_NARPS	P80554	narcissus p
319	13	13.1	9	1	UTAG_HUMAN	P30092	homo sapien	393	13	13.1	20	1	COG1_CHTOP	P34153	chironocete
320	13	13.1	10	1	AMPN_HELAM	P81731	hellioverpa	394	13	13.1	20	1	COG2_PARCM	P20731	parallithode
321	13	13.1	10	1	BPP_VIPAS	P31351	vipera aspi	395	13	13.1	20	1	COG2_CHTOP	P34154	chironocete
322	13	13.1	10	1	BRK_ONCMY	O9prz1	oncorhynch	396	13	13.1	20	1	COG3_CHTOP	P34155	chironocete
323	13	13.1	10	1	GONI_ALIMI	P37041	alligator m	397	13	13.1	20	1	COGA_PARCM	P20732	parallithode
324	13	13.1	10	1	GONI_CHERP	P80677	chelyosoma	398	13	13.1	20	1			

399	13	13.1	20	1	COGB_PARC	P20733	parathlode	472	12	12.1	9	1	OXYT_EISFO	P42998	eisenia foe
400	13	13.1	20	1	COXA_THOB	P80972	thunus obe	473	12	12.1	9	1	OXYT_OCTVU	P80027	octopus vul
401	13	13.1	20	1	COXN_THOB	P80960	thunus obe	474	12	12.1	9	1	OXYT_RABIT	P32878	oryctolagus
402	13	13.1	20	1	FIBB_ELEMA	P14558	elephas max	475	12	12.1	9	1	OXYT_RAVCL	P42994	reia clavat
403	13	13.1	20	1	KORC_METTM	P80966	methanobact	476	12	12.1	9	1	OXYV_SQUAC	P43000	squalus aca
404	13	13.1	20	1	LEC3_MACPO	P18677	maciura pom	477	12	12.1	10	1	ANGT_BOVIN	P01017	bos taurus
405	13	13.1	20	1	LPTB_BACST	P05658	bacillus st	478	12	12.1	10	1	COXM_RAT	P80413	rattus norv
406	13	13.1	20	1	LPTB_BACST	P23058	bacillus su	479	12	12.1	10	1	COXM_RAT	P11755	locusta mig
407	13	13.1	20	1	LYC_FELCA	P37155	felis silve	480	12	12.1	10	1	CU30_LOCOM	P14148	locusta mig
408	13	13.1	20	1	NEUA_RAT	P29188	rattus norv	481	12	12.1	11	1	CEPI_ACHFU	P22790	achetina fu
409	13	13.1	20	1	RLC1_HALMA	P12740	halorcula	482	12	12.1	11	1	TKNA_RANCA	P83308	oncorhynch
410	13	13.1	20	1	RLC1_HALMA	P05511	sus scrofa	483	12	12.1	11	1	TKNA_RANCA	P22668	rana catesb
411	13	13.1	20	1	TPX_CLOPA	P81361	clostridium	484	12	12.1	12	1	PSP3_PHYPA	P80662	physcomit
412	13	13.1	20	1	VSP1_TRIOR	P20005	trimeresur	485	12	12.1	12	1	TKN_KASSE	P88611	kassina sen
413	13	13.1	21	1	CSP1_STRTX	P16622	streptococc	486	12	12.1	12	1	V23K_WSSV	P82005	white spot
414	13	13.1	21	1	FIBB_BISBO	P14466	bison bonas	487	12	12.1	13	1	AU11_LITRA	P82366	litoria ran
415	13	13.1	21	1	GIG1_SPTOL	P55256	spinnacia ol	488	12	12.1	13	1	EI21_LITRU	P82097	litoria ran
416	13	13.1	21	1	GRX_BUNCN	P58305	dunodosoma	489	12	12.1	13	1	NP2_LYNST	P82098	litoria rub
417	13	13.1	21	1	LEC1_MACPO	P18675	maciura pom	490	12	12.1	13	1	NP2_LYNST	P80179	lymaea sta
418	13	13.1	21	1	MCT3_MOUSE	P21843	mus musculu	491	12	12.1	13	1	UHA1_HUMAN	P80162	lymaea sta
419	13	13.1	21	1	RL5_HALME	P50557	halobacteri	492	12	12.1	13	1	UHA1_HUMAN	P01370	tremella me
420	13	13.1	21	1	THAN_PODMA	P55788	podisus mac	493	12	12.1	13	1	NP5_LYNST	P40928	homo sapien
421	13	13.1	21	1	YELA_METVO	P42017	methanococc	494	12	12.1	14	1	DHSL_HORSE	P01016	equus cabal
422	13	13.1	22	1	AOFA_MOUSE	O64133	mus musculu	495	12	12.1	14	1	HY14_PIG	P17874	anabena cy
423	13	13.1	22	1	CYTB_THETS	P81064	theromyzon	496	12	12.1	14	1	MAST_PARID	P01155	sus scrofa
424	13	13.1	22	1	PAZ_DABRU	P18999	daboia russ	497	12	12.1	14	1	MAST_VESLE	P42716	parapolybia
425	13	13.1	22	1	RL18_HALME	P50561	halobacteri	498	12	12.1	15	1	CDN2_LITGI	P01514	vespula lew
426	13	13.1	22	1	RL5_HALVO	P50559	halobacteri	499	12	12.1	15	1	CHX1_CONGE	P56247	litoria gyl
427	13	13.1	22	1	UC07_MAIZE	P80613	zea mays (m	500	12	12.1	15	1	ESTB_SCHGA	P01519	conus geogr
428	13	13.1	22	1	UVSX_BPT2	O06727	bacterioph	501	12	12.1	15	1	SCOT_RAT	P81011	schizaphis
429	13	13.1	22	1	YOKR_CABEL	O09290	caenorhabdi	502	12	12.1	15	1	MAST_PARID	P80263	solanum tub
430	13	13.1	23	1	CLVB_STYCL	P80711	styela clav	503	12	12.1	15	1	CDN2_LITGI	P01514	vespula lew
431	13	13.1	23	1	CR42_LITCE	P56242	litoria cae	504	12	12.1	15	1	CHX1_CONGE	P56247	litoria gyl
432	13	13.1	23	1	CR42_LITCE	P56242	litoria cae	505	12	12.1	15	1	ESTB_SCHGA	P01519	conus geogr
433	13	13.1	23	1	POQA_KLEPN	P27503	klepsidella	506	12	12.1	15	1	LPL_THETH	P81011	schizaphis
434	13	13.1	23	1	PS4_PSEPD	P83191	pseudis par	507	12	12.1	15	1	NUO3_SOLTU	P80263	solanum tub
435	13	13.1	23	1	RL5_HALHA	P50566	halobacteri	508	12	12.1	15	1	SCOT_RAT	P01155	rattus norv
436	13	13.1	23	1	UHA4_HUMAN	P49289	homo sapien	509	12	12.1	16	1	BAIL_EUBSP	P80623	zea mays (m
437	13	13.1	24	1	ACHA_ELEEL	P09688	electrophor	510	12	12.1	16	1	CAT9_FASHE	P32371	eubacterium
438	13	13.1	24	1	CAMT_PINPS	P81081	pinus pinas	511	12	12.1	16	1	DHE2_THOUT	P80553	fasciola he
439	13	13.1	24	1	CH60_ACTICA	P81874	actinetobact	512	12	12.1	16	1	FIBB_FOULS	P20016	thunus thy
440	13	13.1	24	1	DLAA_AMYME	P80413	amycolalops	513	12	12.1	16	1	FIBB_HYULA	P14445	equus asinu
441	13	13.1	24	1	ODPB_BOVIN	P11966	bos taurus	514	12	12.1	16	1	FIBB_HYULA	P14445	equus asinu
442	13	13.1	24	1	PS1_PSEPD	P83188	pseudis par	515	12	12.1	16	1	FIBB_HYULA	P14445	equus asinu
443	13	13.1	24	1	PS2_PSEPD	P83189	pseudis par	516	12	12.1	16	1	FIBB_HYULA	P14445	equus asinu
444	13	13.1	24	1	RAN_XENLA	P52301	xenopus lae	517	12	12.1	16	1	KTTC_AREMA	P11917	arenicola m
445	13	13.1	25	1	VGT_BPAL3	P80766	bacterioph	518	12	12.1	16	1	ODPB_SOLTU	P81419	solanum tub
446	13	13.1	25	1	ACP_ERYLO	P80919	erythrobact	519	12	12.1	16	1	RBL_CAPAN	P27063	capicum an
447	13	13.1	25	1	DNAR_ACTICA	P81875	actinetobact	520	12	12.1	16	1	RBL_CUCSA	P27064	cucumis sat
448	13	13.1	25	1	FLB3_TREHY	P80161	treponema h	521	12	12.1	17	1	BOL1_MEGPE	P27067	vigna sinen
449	13	13.1	25	1	K6P2_THETH	P21778	thermus lthe	522	12	12.1	17	1	BOL2_MEGPE	P10521	megabombus
450	13	13.1	25	1	NCP_PIG	P80552	sus scrofa	523	12	12.1	17	1	BOL3_MEGPE	P07494	megabombus
451	13	13.1	25	1	PRLA_ACHLY	P27459	achromobact	524	12	12.1	17	1	UP33_UPEMJ	P82041	upetroleia t
452	13	13.1	25	1	RL41_AGABI	P78569	agarcia bi	525	12	12.1	18	1	UP34_UPEMJ	P82041	upetroleia m
453	13	13.1	25	1	RL41_SCHPO	O94710	schizosacch	526	12	12.1	18	1	AHD2_TETPY	P33430	tetrahymena
454	13	13.1	25	1	RL41_YEAST	P23356	bos taurus	527	12	12.1	18	1	FMPL_ECOLI	P33430	tetrahymena
455	13	13.1	25	1	UUBL_BOVIN	P09684	gadus morhu	528	12	12.1	18	1	SFAH_HRIAN	P81098	heliathanus
456	13	13.1	25	1	VIP_GADMO	P08497	bacillus su	529	12	12.1	18	1	UC21_KLEAE	P46155	klebsiella
457	12.5	12.6	5	1	UPO1_MOUSE	P38639	mus musculu	530	12	12.1	19	1	CAT3_FASHE	P80532	fasciola he
458	12	12.1	5	1	TY51_LITRU	P82065	litoria rub	531	12	12.1	19	1	CXR_CONTU	P58811	conus tulip
459	12	12.1	7	1	UHI1_RAT	P56576	rattus norv	532	12	12.1	19	1	FTRA_AVTAM	P14440	antilocapra
460	12	12.1	7	1	UHI1_RAT	P82152	cydia pomon	533	12	12.1	19	1	FMOL_CAVPO	P49328	cavia porce
461	12	12.1	8	1	ALLI_CYPDPO	P56575	rattus norv	534	12	12.1	19	1	MDH_BREDE	P33736	escherichia
462	12	12.1	8	1	UHO9_RAT	P05486	conus geogr	535	12	12.1	19	1	MDH_BREDE	P80542	brevundimon
463	12	12.1	9	1	COMO_CONGE	P05487	conus stria	536	12	12.1	19	1	MDH_BREDE	P80542	brevundimon
464	12	12.1	9	1	DNF1_LOCM1	P16339	locusta mig	537	12	12.1	19	1	MDH_SHRON	P82177	shewanella
465	12	12.1	9	1	ISOT_CYPICA	P42993	cyprinus ca	538	12	12.1	19	1	MTRH_TRISP	P81329	trichinella
466	12	12.1	9	1	NER_HV128	P12881	human immun	539	12	12.1	19	1	OILA_OPHNA	P81383	ophthophagus
467	12	12.1	9	1	OXYA_SCTCA	P42996	scyllorhinu	540	12	12.1	19	1	SCX6_TITBA	P24365	streptococc
468	12	12.1	9	1	OXYA_SCTCA	P42997	scyllorhinu	541	12	12.1	19	1	ATP4_SPTOL	P80085	spinnacia ol
469	12	12.1	9	1	OXYF_SQUAC	P42997	scyllorhinu	542	12	12.1	20	1	CAOS_RAT	P19633	rattus norv
470	12	12.1	9	1	OXYT_CYPCA	P23879	cyprinus ca	543	12	12.1	20	1	COGC_PARC	P20734	parathlode
471	12	12.1	9	1	OXYT_CYPCA	P23879	cyprinus ca	544	12	12.1	20	1	COGC_PARC	P20734	parathlode

545	12	12.1	20	1	COX2_OMCY	P80335 oncorhynch	618	11	11.1	10	1	AH3_PRUSE	P29261 prunus sero
546	12	12.1	20	1	CRIC_SPIOT	P30806 spirocha ol	619	11	11.1	10	1	AKH3_LOCM1	P81626 locusta mig
547	12	12.1	20	1	CS21_STRPR	P81621 streptococ	620	11	11.1	10	1	COXH_OMCY	P80331 oncorhynch
548	12	12.1	20	1	DNK1_MYCAV	P80462 mycobacteri	621	11	11.1	10	1	GAU1_HUMAN	P01358 homo sapien
549	12	12.1	20	1	LECB_TIRIO	P36231 liris holian	622	11	11.1	10	1	SP34_DICMU	P81545 dicystostei1
550	12	12.1	20	1	PCR_BACCE	P83075 bacillus ce	623	11	11.1	10	1	SYR_CANUP	Q46464 campylobact
551	12	12.1	20	1	TEMA_ACTTE	P30833 actinia ten	624	11	11.1	10	1	TKNB_CHICK	P18581 gallus gall
552	12	12.1	20	1	TRYL_ECOLI	P33789 escherichia	625	11	11.1	10	1	TKU2_UREUN	P40752 urechis uni
553	12	12.1	20	1	TRYL_STRX	P30470 streptomyce	626	11	11.1	10	1	TRP5_LEUMA	P81737 leucophaea
554	12	12.1	20	1	VR90_BOREE	P81549 bordetella	627	11	11.1	10	1	TRP7_LEUMA	P81740 leucophaea
555	12	12.1	21	1	ATPB_PHYRA	P80568 physconitre	628	11	11.1	10	1	TRP9_LEUMA	P81741 leucophaea
556	12	12.1	21	1	CHIC_PEA	P31233 pisum sativ	629	11	11.1	10	1	TRP4_HUMAN	P30090 homo sapien
557	12	12.1	21	1	LPT_ECOLI	P30359 escherichia	630	11	11.1	10	1	UPA4_HUMAN	P30094 homo sapien
558	12	12.1	21	1	MDR_RHOA	P80458 rhodopseudo	631	11	11.1	10	1	UPA8_HUMAN	P82089 litoria cit
559	12	12.1	21	1	MISG_MISAN	P81474 misgurnus a	632	11	11.1	11	1	CA31_LITCI	P82090 litoria cit
560	12	12.1	21	1	PSBF_SYNU	P12239 synchococc	633	11	11.1	11	1	CA32_LITCI	P56571 rattus norv
561	12	12.1	21	1	SP13_SOLU	P58516 solanum tub	634	11	11.1	11	1	ES1_RAT	P49820 canis fami1
562	12	12.1	22	1	CR32_LITCE	P56239 litoria cae	635	11	11.1	11	1	NUHM_CANPA	P49820 canis fami1
563	12	12.1	22	1	CR33_LITCE	P56240 litoria cae	636	11	11.1	11	1	T2P1_PROVU	P31031 proteus vul
564	12	12.1	22	1	CR1_CLOPA	P81357 clostridium	637	11	11.1	11	1	TKC2_CALVO	P41518 calliphora
565	12	12.1	22	1	HS71_LEIRA	P55938 leishmania	638	11	11.1	11	1	TKN1_ELEMO	P01293 eliedone mos
566	12	12.1	22	1	IF2G_PIG	P20461 sus scrofa	639	11	11.1	12	1	FAR1_CALVO	P41869 calliphora
567	12	12.1	22	1	LPI_TRIMA	P24335 trimeresuru	640	11	11.1	12	1	GRAR_RANRU	P40754 rana rugosa
568	12	12.1	22	1	LPI_TRIMA	P58930 trimeresuru	641	11	11.1	12	1	LM71_LOCM1	P22395 locusta mig
569	12	12.1	22	1	LPI_CORGL	P42456 corynebacte	642	11	11.1	12	1	REF1_CONSP	P58805 conus spuri
570	12	12.1	22	1	LPT_SRRMA	Q84208 serratia ma	643	11	11.1	12	1	TKN2_KASMA	P08614 kassina mac
571	12	12.1	22	1	MOT1_CANPA	P19863 canis fami1	644	11	11.1	12	1	UR2A_CATCO	P04558 catostomus
572	12	12.1	22	1	PHAI_BOVIN	P55930 bos taurus	645	11	11.1	12	1	UR2B_CITCA	P04561 cyprinus ca
573	12	12.1	23	1	CR43_LITCE	P56244 litoria cae	646	11	11.1	13	1	AH4_PRUSE	P23262 pinus sero
574	12	12.1	23	1	CKCV_CONTE	P58845 conus texti	647	11	11.1	13	1	BLAC_STRGR	P81173 streptomyc
575	12	12.1	23	1	GLNA_PHOLP	P20479 phormidium	648	11	11.1	13	1	BP37_LEUMA	P40754 rana rugosa
576	12	12.1	24	1	BRIA_RANES	P40835 rana escul	649	11	11.1	13	1	CPI_APLCA	Q10998 alypsia cal
577	12	12.1	24	1	COXC_THUOB	P80973 thunnus obe	650	11	11.1	13	1	CRBL_ICASP	P17237 icaria sp.
578	12	12.1	24	1	FLRE_RANCA	P55736 rana catesb	651	11	11.1	13	1	ECDE_LYMDI	P80941 lymantria d
579	12	12.1	24	1	FRB4_LITIN	P82032 litoria inf	652	11	11.1	13	1	LMAI_LOCM1	P38496 locusta mig
580	12	12.1	24	1	HEMT_LITNE	P23543 litoria ree	653	11	11.1	13	1	LPNA_PORCI	P81411 porphyromon
581	12	12.1	24	1	HS9B_RABIT	P30947 otycolagus	654	11	11.1	13	1	NEUT_CAVPO	P32660 capra porce
582	12	12.1	24	1	KPKY_CLOPA	P81344 clostridium	655	11	11.1	13	1	NPI_LYMSY	P80178 lymnaea sta
583	12	12.1	24	1	LPBR_STRPR	P54540 streptomyc	656	11	11.1	13	1	PHGR_FUBOX	P57793 bacterium
584	12	12.1	24	1	PA24_TRIST	P8895 trimeresuru	657	11	11.1	13	1	PSAE_PEA	P20118 pisum sativ
585	12	12.1	24	1	PEP1_ASPPG	P55749 aspergillus	658	11	11.1	13	1	UP71_LITWE	P82050 litoria ewi
586	12	12.1	24	1	POOA_ACTCA	P25177 actinobact	659	11	11.1	14	1	CAT2_FASHE	P80342 fasciola he
587	12	12.1	24	1	POQA_PSEEL	P56233 litoria spl	660	11	11.1	14	1	COCO_LIMPO	P35586 limulus pol
588	12	12.1	25	1	CR21_LITSP	P56233 litoria cae	661	11	11.1	14	1	GLPK_STRGR	P25013 streptomyc
589	12	12.1	25	1	CR23_LITCE	P56236 litoria cae	662	11	11.1	14	1	HCVI_MESCR	Q10583 megastura c
590	12	12.1	25	1	CR24_LITCE	P56236 litoria cae	663	11	11.1	14	1	KARA_BROPL	P22442 bromella pl
591	12	12.1	25	1	CYC4_VIBRI	P80891 vibrio fisc	664	11	11.1	14	1	LPBR_BACLI	Q04303 bacillus ii
592	12	12.1	25	1	GBX1_MOUSE	P82976 mus musculu	665	11	11.1	14	1	MAST_POLJA	P01517 polistes ja
593	12	12.1	25	1	LE01_BIOGL	P80742 biomphalari	666	11	11.1	14	1	MAST_VESMA	P04205 vespa manda
594	12	12.1	25	1	MDH_PHEIM	P19980 phenylbact	667	11	11.1	14	1	MAST_VESXA	P01515 vespa xanth
595	12	12.1	25	1	MT_NENCIR	P02807 neurospora	668	11	11.1	14	1	SODN_STRGR	P80732 streptomyc
596	12	12.1	25	1	PAZH_BOTSC	P80963 bochrlechis	669	11	11.1	15	1	4BKD_BACCE	P80173 bacillus ce
597	12	12.1	6	1	E101_LITRU	P82096 litoria rub	670	11	11.1	15	1	ACEA_ACTCA	P28467 actinobact
598	12	12.1	7	1	E105_LITRU	P82101 litoria rub	671	11	11.1	15	1	ACT_PIPNS	P81085 pinus pinas
599	12	12.1	7	1	UC24_MAIZE	P80630 zea mays (m	672	11	11.1	15	1	AH2_PRUSE	P29260 pinus sero
600	12	12.1	7	1	UF04_MOUSE	P36642 mus musculu	673	11	11.1	15	1	ARCA_STRPS	P58827 streptococ
601	12	12.1	8	1	ALU5_CYPDO	P82156 cydia pomon	674	11	11.1	15	1	CHIL_PEA	P21225 pisum sativ
602	12	12.1	8	1	CCKN_MACEU	P30369 macropus eu	675	11	11.1	15	1	COXI_THUOB	P80978 thunnus obe
603	12	12.1	8	1	GLUR_HUMAN	P07729 homo sapien	676	11	11.1	15	1	FTBA_SYNCA	P14463 syncerus ca
604	12	12.1	8	1	NS3_MYCTU	P81152 mycobacteri	677	11	11.1	15	1	ITRB_AUBJU	P24927 albizia ju
605	12	12.1	9	1	COXE_THUOB	P80975 thunnus obe	678	11	11.1	15	1	LECI_PSOIC	P23582 psophocarpu
606	12	12.1	9	1	DSIP_RABIT	P01158 otycolagus	679	11	11.1	15	1	LPE_ECOLI	P30357 escherichia
607	12	12.1	9	1	FAR2_CALVO	P41857 calliphora	680	11	11.1	15	1	MORA_MENTE	P22395 locusta mig
608	12	12.1	9	1	FAR3_CALVO	P41858 calliphora	681	11	11.1	15	1	MILT_ONCKE	P81037 oncorhynch
609	12	12.1	9	1	FAR4_CALVO	P41859 calliphora	682	11	11.1	15	1	MM01_RAT	P81563 rattus norv
610	12	12.1	9	1	FARA_CALVO	P41865 calliphora	683	11	11.1	15	1	NUO6_SOLJU	P80731 solanum tub
611	12	12.1	9	1	FIBB_ERYPA	P19346 erythrocebu	684	11	11.1	15	1	R13A_SPIOL	P82454 spinacia ol
612	12	12.1	9	1	FIBB_TREHY	P19347 erythrocebu	685	11	11.1	15	1	R131_STRAU	Q9X320 streptomyc
613	12	12.1	9	1	FLA2_TREHY	P80159 treponema h	686	11	11.1	15	1	THL_CLOPA	P81347 clostridium
614	12	12.1	9	1	LM73_LOCM1	P41489 locusta mig	687	11	11.1	15	1	UC01_MAIZE	P80607 zea mays (m
615	12	12.1	9	1	TRP4_LEUMA	P81736 leucophaea	688	11	11.1	15	1	UC06_MAIZE	P80612 zea mays (m
616	12	12.1	9	1	ULAK_MOUSE	P90031 mus musculu	689	11	11.1	15	1	UC13_MAIZE	P80619 zea mays (m
617	12	12.1	9	1	UPA7_HUMAN	P30093 homo sapien	690	11	11.1	15	1	UC29_MAIZE	P80635 zea mays (m

691	11	11.1	15	1	VAA3_RHOA	Q02006 rhodopseudo	764	11	11.1	20	1	VMO2_CHICK	Q9ps49 gallus gall
692	11	11.1	16	1	AH1_PROSE	P22259 prunus sero	765	11	11.1	21	1	BRX_ATRBI	P80163 atractaspis
693	11	11.1	16	1	ALR3_PSEPU	P17916 pseudomonas	766	11	11.1	21	1	CAKT_CONIU	P17684 conus tulip
694	11	11.1	16	1	CT11_LITCI	P81835 litorea cit	767	11	11.1	21	1	FIBB_ANTAM	P14465 antilocapra
695	11	11.1	16	1	CT12_LITCI	P81840 litorea cit	768	11	11.1	21	1	FIBB_SYNCA	P14481 synecrus ca
696	11	11.1	16	1	CT13_LITCI	P81846 litorea cit	769	11	11.1	21	1	MDH_BURCE	P80537 burkholderi
697	11	11.1	16	1	CXAI_CONEP	P56638 conus episc	770	11	11.1	21	1	MDH_PSEIN	P80538 pseudomonas
698	11	11.1	16	1	CXAA_CONEP	P50984 conus penna	771	11	11.1	21	1	MDP2_SOLUN	P81206 solanum tub
699	11	11.1	16	1	FIRA_TAPTE	P14536 tapirus ter	772	11	11.1	21	1	OMP1_HABPR	P81421 solanum tub
700	11	11.1	16	1	FOR2_MYRGU	P81437 myrmecia gu	773	11	11.1	21	1	PSAL_STYNE	P81069 haemophilus
701	11	11.1	16	1	HP28_SAREP	P80744 sarcophaga	774	11	11.1	21	1	REF1_STRSQ	P31084 synecchococ
702	11	11.1	16	1	LE05_BIOGL	P80744 blomphalari	775	11	11.1	21	1	SCIB_BPT5	P37046 streptomyc
703	11	11.1	16	1	LPK1_LOCM1	P20404 locusta mig	776	11	11.1	21	1	SRTD_ATREN	P23208 bacterioph
704	11	11.1	16	1	OD02_BOVIN	P11179 bos taurus	777	11	11.1	21	1	TL13_SPIOL	P13211 atractaspis
705	11	11.1	16	1	PA2_NAASP	Q10756 naia sputat	778	11	11.1	21	1	XYNA_DICB4	P82661 spiracula ol
706	11	11.1	16	1	RL6_VIBPR	Q56715 vibrio prot	779	11	11.1	21	1	APC1_MACPA	P80718 dictyoglomu
707	11	11.1	16	1	VPR_HV1S3	P19555 human immun	780	11	11.1	22	1	APC1_MACPA	P18657 macaca fasc
708	11	11.1	16	1	YMOE_PSEPU	Q02210 pseudomonas	781	11	11.1	22	1	CO4_CAVPO	P19069 cavia porce
709	11	11.1	17	1	A43K_MYCBO	P80069 mycobacteri	782	11	11.1	22	1	CR31_LITSP	P56328 litorea spl
710	11	11.1	17	1	ACTE_SOYBN	P1986 glycine max	783	11	11.1	22	1	DNIV_BPD10	Q38199 bacterioph
711	11	11.1	17	1	DNK_MYCSM	P80692 mycobacteri	784	11	11.1	22	1	MLP_RANFE	P56924 rana temp
712	11	11.1	17	1	RUBR_CHLJE	P58025 chlorobium	785	11	11.1	22	1	MOT1_CHICK	Q9prp6 gallus gall
713	11	11.1	17	1	SRY_URSAR	P36396 ursus arcto	786	11	11.1	22	1	VLIG_RABVA	P15199 rabies viru
714	11	11.1	17	1	TAC1_TACGI	P23684 tachyples	787	11	11.1	22	1	YHVA_LACHE	P22296 lactobacill
715	11	11.1	17	1	TAC2_TACGI	P18252 tachyples	788	11	11.1	22	1	CYSP_TRIFO	P33403 tritrichomo
716	11	11.1	18	1	AL12_CYDPO	P83153 cydia pomon	789	11	11.1	23	1	GP50_BPSP1	Q48404 bacterioph
717	11	11.1	18	1	CT1A_LITCI	P81838 litorea cit	790	11	11.1	23	1	MU12_LITGE	P82067 litorea gen
718	11	11.1	18	1	CT1B_LITCI	P81839 litorea cit	791	11	11.1	23	1	NO05_SOLLU	P80262 solanum tub
719	11	11.1	18	1	CT1C_LITCI	P81844 litorea cit	792	11	11.1	23	1	RL10_ENTCL	Q47608 enterobacte
720	11	11.1	18	1	CT1D_LITCI	P81845 litorea cit	793	11	11.1	23	1	RL19_PETUY	P18550 pentula hyb
721	11	11.1	18	1	FIBB_ANAPL	P12802 anas platyr	794	11	11.1	24	1	BRL_RANBP	P32423 rana brevip
722	11	11.1	18	1	FIXA_RHILE	P14313 rhizobium l	795	11	11.1	24	1	CH60_HELVY	P26317 heliothis v
723	11	11.1	18	1	HEMH_THETS	P80155 thermomyzom	796	11	11.1	24	1	CLPE_HORVU	P48863 hordium vul
724	11	11.1	18	1	LYC_ESTAC	P82175 estiermyzom	797	11	11.1	24	1	CLPE_HORVU	P56231 litorea xan
725	11	11.1	18	1	MCPE_METRE	P22949 methanosarc	798	11	11.1	24	1	CR16_LITXA	P81251 litorea chl
726	11	11.1	18	1	MOD1_LITGE	P82066 litorea gen	799	11	11.1	24	1	CR19_LITCH	P81252 litorea chl
727	11	11.1	18	1	OBP_LYMDI	P34173 lymantria d	800	11	11.1	24	1	CSMB_PELDU	P15526 pelodictyon
728	11	11.1	18	1	PEP1_LIMPO	P14215 limulus pol	801	11	11.1	24	1	DHE3_PYRMO	Q09115 pyrococcus
729	11	11.1	18	1	TKN2_SCYCA	P08609 scyllorhinu	802	11	11.1	24	1	HEM4_LITNE	P23534 lingua ree
730	11	11.1	19	1	AL12_HORSE	P81217 equus cabal	803	11	11.1	24	1	LEC_CROUY	P16332 crotalaria
731	11	11.1	19	1	CH10_CLOPA	P81338 clostridium	804	11	11.1	24	1	RS5_VIBPR	P52856 vibrio prot
732	11	11.1	19	1	COOR_SARBU	Q09148 sarcophaga	805	11	11.1	25	1	ANDT_ANDAU	P56644 antioctonus
733	11	11.1	19	1	DURR_SARGV	P36504 streptococ	806	11	11.1	25	1	ANT3_MESAU	P81050 mesocricetu
734	11	11.1	19	1	DURR_SARGV	P36503 streptococ	807	11	11.1	25	1	APRY_SOLCU	P80497 solanum tub
735	11	11.1	19	1	DURC_STRGP	P36503 streptococ	808	11	11.1	25	1	AU52_LITRA	P82402 litorea ran
736	11	11.1	19	1	FIBB_RANTA	P14662 raungler la	809	11	11.1	25	1	BGBP_PENYA	P81162 penaeus van
737	11	11.1	19	1	FIBB_PIG	P14477 sus scrofa	810	11	11.1	25	1	CHIV_CARPA	P81241 carlica papa
738	11	11.1	19	1	FIBB_VOLVU	P14482 vulpes vulp	811	11	11.1	25	1	CR11_LITSP	P56226 litorea spl
739	11	11.1	19	1	H3_NARPS	P80553 narciassus p	812	11	11.1	25	1	CR12_LITCE	P56227 litorea cae
740	11	11.1	19	1	ITHA_PERAM	P19586 periplaneta	813	11	11.1	25	1	CR13_LITCE	P56228 litorea cae
741	11	11.1	19	1	LANC_STRSO	P36655 streptococ	814	11	11.1	25	1	CR14_LITGE	P56229 litorea gll
742	11	11.1	19	1	LEPM_STRAU	P03063 streptococ	815	11	11.1	25	1	CR15_LITGE	P56230 litorea cae
743	11	11.1	19	1	PHSL_DESBN	P13066 desulfovibr	816	11	11.1	25	1	CR16_LITSP	P82104 litorea spl
744	11	11.1	19	1	PSBM_STYNU	P12312 synecchococ	817	11	11.1	25	1	CX44_CONFU	P55963 conus purpu
745	11	11.1	19	1	PYRB_PSEFL	P56585 pseudomonas	818	11	11.1	25	1	FLAA_TREPH	P21963 treponema p
746	11	11.1	19	1	TRBP_KLEAE	P14552 klebsiella	819	11	11.1	25	1	IRBP_PIG	P12662 sus scrofa
747	11	11.1	19	1	UKAI_HUMAN	P31940 homo sapien	820	11	11.1	25	1	LYC_ASTRU	P37715 agaricus ru
748	11	11.1	20	1	APAI_ERVPA	P18647 erythrocebu	821	11	11.1	25	1	MT_AGABI	P04338 agaricus bl
749	11	11.1	20	1	BIP_PHAVU	P80089 phaseolus v	822	11	11.1	25	1	NEOU_RABIT	P34965 oryctolagus
750	11	11.1	20	1	CATL_FASHE	Q00993 fasciola he	823	11	11.1	25	1	SPFG_PSEUS	P82357 pseudocanth
751	11	11.1	20	1	COGA_FASHE	P34156 chionocete	824	11	11.1	25	1	YX8L_ODOSI	P49834 odontella s
752	11	11.1	20	1	COXM_THUOB	P80981 thunnus ode	825	11	11.1	25	1	BOS1_HUMAN	P02721 homo sapien
753	11	11.1	20	1	ELAS_GADMO	P32197 gadus morhu	826	11	10.1	4	1	ACEPH_RABIT	P25134 oryctolagus
754	11	11.1	20	1	FIBB_FELIS	P14469 felis silve	827	11	10.1	6	1	ASPF_LACSN	P82645 lactobacill
755	11	11.1	20	1	GTS2_ASCSU	P48429 ascaris suu	828	11	10.1	6	1	TRP1_PSEPU	P36960 pseudomonas
756	11	11.1	20	1	NLT1_HELIAN	P82007 helianthus	829	11	10.1	7	1	LANC_CARUI	P42964 leptinotars
757	11	11.1	20	1	PEPT_FUSNP	P19052 fusobacteri	830	11	10.1	7	1	MMN1_ACHRU	P35919 achelina fu
758	11	11.1	20	1	PSBH_SYNUV	P81669 styela clay	831	11	10.1	7	1	WM42_ACHRU	P35920 porphyromon
759	11	11.1	20	1	STVA_STYCL	P82682 spinacia ol	832	11	10.1	8	1	B44K_PORCI	P21140 leucophaea
760	11	11.1	20	1	TL14_SPIOL	P82336 spinacia ol	833	11	10.1	8	1	LCK1_LEUMA	P19989 leucophaea
761	11	11.1	20	1	UCRO_EDUAR	P81247 equisetum a	834	11	10.1	8	1		
762	11	11.1	20	1			835	11	10.1	8	1		
763	11	11.1	20	1	UN05_PINPS	P81674 pinus pinas	836	11	10.1	8	1		

837	10	10.1	8	1	LPK_LEUMA	P13049	leucophaea	910	10	10.1	15	1	CX3B_CONOU	P58842	conus querc
838	10	10.1	8	1	RS1_ERWCH	P37985	erwinia chr	910	10	10.1	15	1	FKB7_PINS	P81104	pinus pinas
839	10	10.1	8	1	RS7_MYCIT	P35564	mycobacteri	911	10	10.1	15	1	FRE2_LITIN	P82022	litorea inf
840	10	10.1	9	1	FAR6_CALVO	P41861	calliphora	912	10	10.1	15	1	GR78_HORSE	P16392	equus cabal
841	10	10.1	9	1	FAR7_CALVO	P41862	calliphora	913	10	10.1	15	1	LCK_DROME	P61829	drosophila
842	10	10.1	9	1	FAR9_ASCSU	P43172	ascaris suu	914	10	10.1	15	1	LEC2_PSOSC	P22559	psophocarpa
843	10	10.1	9	1	HOTU_KLEAE	P12381	klebsiella	915	10	10.1	15	1	LEC3_PSOSC	P22563	psophocarpu
844	10	10.1	9	1	MGMT_BOVIN	P29177	bos taurus	916	10	10.1	15	1	MALT_BACPO	P80072	bacillus th
845	10	10.1	9	1	PKR1_PERAM	P82691	periplaneta	917	10	10.1	15	1	PKKH_PHYPA	P80659	physcomitre
846	10	10.1	9	1	UN19_CLOPA	P81355	clostridium	918	10	10.1	15	1	PH3_PRUSE	P29265	prunus sero
847	10	10.1	9	1	XYLA_SRSO	P19149	streptomyce	919	10	10.1	15	1	RRGG_CARCR	P21586	carella car
848	10	10.1	9	1	BPP2_BOTJA	P30422	bothrops in	920	10	10.1	15	1	SODP_PINS	P811082	pinus pinas
849	10	10.1	10	1	BPP2_BOTJA	P30422	bothrops in	921	10	10.1	15	1	TRPA_LEUMA	P10753	leucophaea
850	10	10.1	10	1	COXA_OMCMY	P80328	oncorhynchu	922	10	10.1	15	1	UC14_MAIZE	P80626	zea mays (m
851	10	10.1	10	1	COXO_RABIT	P80336	oryctolagus	923	10	10.1	15	1	UC20_MAIZE	P80626	zea mays (m
852	10	10.1	10	1	ESTR_SCHGA	P81012	schizaphis	924	10	10.1	15	1	UC25_MAIZE	P80633	zea mays (m
853	10	10.1	10	1	FARC_CALVO	P41867	calliphora	925	10	10.1	15	1	UC27_MAIZE	P34938	hordeum vul
854	10	10.1	10	1	FIBB_CERSI	P14537	ceratotheri	926	10	10.1	15	1	UE15_HORVU	P17338	morganelia
855	10	10.1	10	1	GSO9_BACSU	P80343	bacillus su	927	10	10.1	15	1	URE2_MORMO	P13436	ratius norv
856	10	10.1	10	1	MOSO_CLYJA	P19862	clypeaster	928	10	10.1	16	1	CERB_RAT	P56639	conus aulic
857	10	10.1	10	1	PORB_METJM	P80301	methanobact	929	10	10.1	16	1	CXA1_CONAL	P56636	conus magus
858	10	10.1	10	1	RL16_ACHLA	P29221	acholeplasm	930	10	10.1	16	1	CXA2_CONAL	P56641	conus aulic
859	10	10.1	10	1	TKNK_PIG	P01392	sus scrofa	931	10	10.1	16	1	CXA3_CONAL	P14535	ceratotheri
860	10	10.1	10	1	TKS1_AEDAE	P42634	aedes aegypt	932	10	10.1	16	1	FIBA_FELCA	P14530	telis silve
861	10	10.1	10	1	TKS2_AEDAE	P42635	aedes aegypt	933	10	10.1	16	1	FIBA_FELCA	P14455	mandillius
862	10	10.1	10	1	BPP3_BOTIN	P30423	bothrops in	934	10	10.1	16	1	H5_CORJA	P18638	colurnix co
863	10	10.1	11	1	BPP4_BOTIN	P30424	bothrops in	935	10	10.1	16	1	HPFG_ACICA	P81876	acinetobact
864	10	10.1	11	1	BPP4_AGKHA	P01021	agkistrodon	936	10	10.1	16	1	LEO6_BIOGL	P80745	biomphalari
865	10	10.1	11	1	PKR1_PERAM	P41837	periplaneta	937	10	10.1	16	1	PGTL_PELAC	P80563	pelobacter
866	10	10.1	11	1	REAL_LITRU	P82074	litorea rub	938	10	10.1	16	1	PH2_PRUSE	P23264	prunus sero
867	10	10.1	11	1	TIN1_HOPTI	P82651	hoplobatrach	939	10	10.1	16	1	TRYP_FELCA	P81071	telis silve
868	10	10.1	11	1	TIN4_HOPTI	P82654	hoplobatrach	940	10	10.1	16	1	FLAM_AZOC	P14460	sus scrofa
869	10	10.1	11	1	TKN3_PSEGU	P42988	pseudophryna	941	10	10.1	17	1	FIBA_PIG	P23002	azotobacter
870	10	10.1	11	1	CALM_TERTH	O05055	tetrahymena	942	10	10.1	17	1	TRYP_FELCA	P56675	platytrepia
871	10	10.1	12	1	CD14_LITXA	P56246	litorea xan	943	10	10.1	17	1	FLAM_AZOC	O01621	ratius norv
872	10	10.1	12	1	CXST_CONTE	P58846	conus texti	944	10	10.1	17	1	ICK_RAT	O36834	trichophyto
873	10	10.1	12	1	HCVB_MEGCR	Q10564	megathura c	945	10	10.1	17	1	NUAM_TIRIRU	P27642	baecillus li
874	10	10.1	12	1	LICH_BACLI	P82907	baecillus li	946	10	10.1	17	1	SPS1_BACLI	P81666	pinus pinas
875	10	10.1	12	1	LICH_BACLI	P82619	periplaneta	947	10	10.1	17	1	TPIS_PINS	P82032	uperoleia i
876	10	10.1	12	1	PPK4_PPERU	P82650	periplaneta	948	10	10.1	17	1	UP31_UEPIN	P82033	uperoleia i
877	10	10.1	12	1	PPK2_PPERU	P81555	periplaneta	949	10	10.1	17	1	UP32_UEPIN	P82044	uperoleia m
878	10	10.1	12	1	TIN2_HOPTI	P82652	hoplobatrach	950	10	10.1	17	1	UP37_UEPMJ	P82035	uperoleia m
879	10	10.1	12	1	TIN3_HOPTI	P82653	hoplobatrach	951	10	10.1	17	1	UP41_UEPIN	P17961	trypanosoma
880	10	10.1	12	1	UDAL_MOUSE	P99032	mus musculu	952	10	10.1	17	1	YALA_TRYBB	P01209	padatus bo
881	10	10.1	12	1	XYLA_STRVN	P14405	streptomyce	953	10	10.1	17	1	DRPH_PANBO	P08871	uca pugilati
882	10	10.1	12	1	VZPY_ECOLI	P17221	vespa tropi	954	10	10.1	18	1	FIBA_CAMDR	P14454	lama glama
883	10	10.1	13	1	CRBL_VESTR	P28489	bos taurus	955	10	10.1	18	1	HEX_ADECU	P35985	canine aden
884	10	10.1	13	1	CRTC_BOVIN	P23416	rana esculie	956	10	10.1	18	1	PCG6_PACGO	P82419	pachycondyl
885	10	10.1	13	1	HPB9_RANES	P20304	sus scrofa	957	10	10.1	18	1	PHPT_PACSE	P25271	pseudatelia
886	10	10.1	13	1	IDHC_PIG	P20011	trameles ve	958	10	10.1	18	1	RIP_SIRGR	P83323	sirattia gr
887	10	10.1	13	1	LIGA_TRAVE	P41490	locusta mig	959	10	10.1	18	1	RL24_SERMA	P49624	serratia ma
888	10	10.1	13	1	LMF4_LOCM1	P13724	gallus gall	960	10	10.1	18	1	ATPB_CANFA	P99504	canis famill
889	10	10.1	13	1	NEUT_CHICK	P31745	trichosurus	961	10	10.1	18	1	COXA_ONCMY	P80327	oncorhynchu
890	10	10.1	13	1	NEUT_TRIUV	P31745	trichosurus	962	10	10.1	19	1	COXK_THUOB	P80984	thunnus obe
891	10	10.1	13	1	NP3_LYMST	P80180	lymaea sta	963	10	10.1	19	1	DHAB_COMTE	P80704	comonomas t
892	10	10.1	13	1	PEDI_HYDAT	P80578	hydra atten	964	10	10.1	19	1	ETFA_CLOPA	P81342	clostridium
893	10	10.1	13	1	RPOC_MYCGA	P47716	mycoplasma	965	10	10.1	19	1	FIBA_BISBO	P14441	bison bonas
894	10	10.1	13	1	TEMF_RANTE	P56921	rana tempor	966	10	10.1	19	1	FIBA_MUNMU	P14457	mus mus
895	10	10.1	13	1	UNO2_PINS	P81667	pinus pinas	967	10	10.1	19	1	FLAB_TAPTE	P21986	spirochaeta
896	10	10.1	14	1	ATP6_SPIOL	P80086	spiniacia ol	968	10	10.1	19	1	NUO6_SOLTA	P80729	solannu tub
897	10	10.1	14	1	CRBL_VESOR	P17236	vespa orien	969	10	10.1	19	1	PHLC_STAIN	P80924	staphylococ
898	10	10.1	14	1	MAST_VESOR	P17238	vespa orien	970	10	10.1	19	1	RLIO_CITFR	P43448	citrobacter
899	10	10.1	14	1	MCRX_METTM	P58815	methanobact	971	10	10.1	19	1	TCBI_TRILO	P80070	trichoderma
900	10	10.1	14	1	PH1_PRUSE	P29263	prunus sero	972	10	10.1	19	1	UC31_MAIZE	P80637	zea mays (m
901	10	10.1	14	1	UHA2_CANFA	P99506	canis famill	973	10	10.1	19	1	UP21_UEPIN	P82027	uperoleia i
902	10	10.1	15	1	ATP2_SPIOL	P80083	spiniacia ol	974	10	10.1	19	1	UP22_UEPIN	P82028	uperoleia i
903	10	10.1	15	1	C1O3_RAT	P31720	ratius norv	975	10	10.1	19	1	UP23_UEPIN	P82030	uperoleia i
904	10	10.1	15	1	CDN3_LITGI	P56248	litorea gill	976	10	10.1	19	1	ACPH_BOVIN	P80227	bos taurus
905	10	10.1	15	1	CDN4_LITCE	P82076	litorea cae	977	10	10.1	20	1	CATA_ACIRA	P81422	acinetobact
906	10	10.1	15	1	CDN5_LITCE	P82077	litorea cae	978	10	10.1					
907	10	10.1	15	1	CDN6_LITCE	P82078	litorea cae	979	10	10.1					
908	10	10.1	15	1	CKX_WHEAT	P58763	tritium ae	980	10	10.1					
909	10	10.1	15	1	CX3A_CONOU	P58841	conus querc	981	10	10.1					
								982	10	10.1					

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983 10 10.1 20 1 CD4_SHEEP
984 10 10.1 20 1 GBP_THICU
985 10 10.1 20 1 COX2_THICU
986 10 10.1 20 1 CBP5_PAPSP
987 10 10.1 20 1 CBP5_PAPSP
988 10 10.1 20 1 CBP5_PAPSP
989 10 10.1 20 1 CBP5_PAPSP
990 10 10.1 20 1 CBP5_PAPSP
991 10 10.1 20 1 CBP5_PAPSP
992 10 10.1 20 1 CBP5_PAPSP
993 10 10.1 20 1 CBP5_PAPSP
994 10 10.1 20 1 CBP5_PAPSP
995 10 10.1 20 1 CBP5_PAPSP
996 10 10.1 20 1 CBP5_PAPSP
997 10 10.1 20 1 CBP5_PAPSP
998 10 10.1 20 1 CBP5_PAPSP
999 10 10.1 20 1 CBP5_PAPSP
1000 10 10.1 20 1 CBP5_PAPSP

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ALIGNMENTS

RESULT 1

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UC08_MAIZE STANDARD; PRT; 15 AA.
AC P80614;

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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
DE (Fragment).
OS Zea mays (Maize).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_Taxid=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzel P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.
CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.

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DR Maize-2DPAGE; P80614; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1785 MW; 1978BD1D6AB4D8F8D CRC64;

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Query Match 30.3%; Score 30; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 VPQHE 6
DB 11 VPQHE 15

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RESULT 2

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CP23_SPOER STANDARD; PRT; 23 AA.
AC P56683;

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DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cardioactive peptide CAP23.
DE Spodoptera eridania (Southern armyworm).

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OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Noctuidae; Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_Taxid=37547;
RN [1]
RP SEQUENCE.
RX MEDLINE=99196260; PubMed=1009624;
RA Furuya K., Hackett M., Cirelli M.A., Schegg K.M., Wang H.,
RA Shabanowitz J., Hunt D.F., Schooley D.A.;
RT "A cardioactive peptide from the southern armyworm, Spodoptera
RT eridania.";
RT Peptides 20:53-61(1999).
RT -!- FUNCTION: HAS EXCITATORY EFFECTS ON A SEMI-ISOLATED HEART FROM
RT LARVAL MANDUCA SEXTA, CAUSING AN INOTROPIC EFFECT AT LOW
RT CONCENTRATIONS OF PEPTIDE AND CHRONOTROPIC AND INOTROPIC EFFECTS
RT AT HIGH DOSES.
CC -!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
CC HSSP: 061704; 1B1V.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
FT DISULFID 7 19
SQ SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

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Query Match 30.3%; Score 30; DB 1; Length 23;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 3 PGHERMGGR 12
DB 9 PORYRTADGR 18

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RESULT 3

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PAP1_SPOEX STANDARD; PRT; 23 AA.
AC P30255;

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DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Paralytic peptide I (pp I).
DE Spodoptera exigua (Beet armyworm).
OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Noctuidae; Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_Taxid=7107;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
RA Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
RT Heliothis virescens.";
RL J. Biol. Chem. 266:12873-12877(1991).

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CC -!- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
CC HSSP: 061704; 1B1V.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
KW Hemolymph.
FT DISULFID 7 19
SQ SEQUENCE 23 AA; 2451 MW; 0A96D1F600855AE0 CRC64;

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Query Match 30.3%; Score 30; DB 1; Length 23;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 3 PGHERMGGR 12
DB 9 PORYRTADGR 18

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Db 9 PGYQRTADGR 18

RESULT 4

PAP2_SPOEX STANDARD; PRT; 23 AA.

AC P30257;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Paralytic peptide II (PP II).
OS Spodoptera exiguua (Beet armyworm).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Noctuoidea; Noctuidae; Amphipyridae; Spodoptera.
OX NCBI_TaxID=7107;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=91302298; PubMed=2071576;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
the lepidopteran insects Manduca sexta, Spodoptera exiguua, and
Heliothis virescens.";
RT J. Biol. Chem. 266:12873-12877(1991).
RL -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
CC PIR: D39855; D39855.
DR HSSP: O61704; 1B1V.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
KW Hemolymph.
FT DISULFID
SQ SEQUENCE 23 AA: 2477 MW: 0A96CB4600855AE0 CRC64:

Query Match 30.3%; Score 30; DB 1; Length 23;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGHERMGRGR 12
II::I II
Db 9 PGYQRTADGR 18

RESULT 5

PAP3_SPOEX STANDARD; PRT; 23 AA.

AC P30257;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Paralytic peptide III (PP III).
OS Spodoptera exiguua (Beet armyworm).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Noctuoidea; Noctuidae; Amphipyridae; Spodoptera.
OX NCBI_TaxID=7107;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=91302298; PubMed=2071576;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
the lepidopteran insects Manduca sexta, Spodoptera exiguua, and
Heliothis virescens.";
RT J. Biol. Chem. 266:12873-12877(1991).
RL -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
CC PIR: D39855; D39855.
DR HSSP: O61704; 1B1V.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
KW Hemolymph.
FT DISULFID
SQ SEQUENCE 23 AA: 2524 MW: 2236CB43D0655AFA CRC64:

Query Match 29.3%; Score 29; DB 1; Length 23;
Best Local Similarity 45.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VPGHERMGRGR 12
II::I II
Db 8 IPGYRTADGR 18

RESULT 7

PAP2_HELVI STANDARD; PRT; 23 AA.

AC P30257;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Paralytic peptide II (PP II).
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=91302298; PubMed=2071576;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
the lepidopteran insects Manduca sexta, Spodoptera exiguua, and
Heliothis virescens.";
RT J. Biol. Chem. 266:12873-12877(1991).
RL -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
CC PIR: F39855; F39855.
DR HSSP: O61704; 1B1V.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
KW Hemolymph.
FT DISULFID
SQ SEQUENCE 23 AA: 2524 MW: 2236CB43D0655AFA CRC64:

Query Match 29.3%; Score 29; DB 1; Length 23;
Best Local Similarity 45.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VPGHERMGRGR 12
II::I II
Db 8 IPGYRTADGR 18

RESULT 6

PAP1_HELVI STANDARD; PRT; 23 AA.

AC P30251;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Paralytic peptide I (PP I).
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=91302298; PubMed=2071576;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
the lepidopteran insects Manduca sexta, Spodoptera exiguua, and
Heliothis virescens.";
RT J. Biol. Chem. 266:12873-12877(1991).
RL -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
CC PIR: F39855; F39855.
DR HSSP: O61704; 1B1V.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
KW Hemolymph.
FT DISULFID
SQ SEQUENCE 23 AA: 2524 MW: 2236CB43D0655AFA CRC64:

Query Match 29.3%; Score 29; DB 1; Length 23;
Best Local Similarity 45.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VPGHERMGRGR 12
II::I II
Db 8 IPGYRTADGR 18

DR PROSITE: PS00046; HISTONE_H2A; PARTIAL.
 KM Chromosomal protein; Nucleosome core; Nuclear protein;
 KM DNA-binding; Antibiotic; Fungicide; Acetylation.
 FT NON_TER 1 1
 FT MOD_RES 1 1 ACETYLATION.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1202 MW; 3EF28D9668D87DD8 CRC64;

Query Match 22.2%; Score 22; DB 1; Length 12;
 Best Local Similarity 66.7%; Pred. No. 7.7e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 ERMGREG 11
 11:11
 Db 2 ERVGAG 7

RESULT 14
 TL11_SPTOL STANDARD; PRT; 22 AA.
 P82657;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid lumenal 11 kDa protein (P11) (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RA Kieselbach T., Petersson U., Bystedt M., Schroeder W.P.;
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 CC -1- SIMILARITY: TO A.THALIANA AT2G44920.
 KM Chloroplast; Thylakoid.
 FT NON_TER 22 22
 SQ SEQUENCE 22 AA; 2271 MW; EBFED6814A203F43 CRC64;

Query Match 22.2%; Score 22; DB 1; Length 22;
 Best Local Similarity 36.4%; Pred. NO. 1.5e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 9 GGRRTSSKELA 19
 1:11:11:
 Db 8 GGQVTRGDDLS 18

RESULT 15
 G3P2_JACOR STANDARD; PRT; 25 AA.
 ID 3P22_JACOR
 AC P80447;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (GAPDH) (Fragment).
 OS GAPD OR GAPC.
 OS Jaculus orientalis.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Dipodidae; Dipodinae;
 OC Jaculus.
 NCBI_TaxID=48868;
 RN [1]
 RP SEQUENCE.
 RA MDL:LINE=96139342; PubMed=8547342;
 RA Soukri A., Hafid N., Valverde F., Elkebbaj M.S., Serrano A.;
 RT "Evidence for a posttranslational covalent modification of liver
 RT glyceraldehyde-3-phosphate dehydrogenase in hibernating jerboa
 RT (Jaculus orientalis).";
 RL Biochim. Biophys. Acta 1292:177-187(1996).

CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: cytoplasmic.
 CC -1- PTM: THE HIBERNATING ADULT ISOFORM IS ADP-RIBOSYLATED. THIS
 CC ACCOUNTS FOR 2-3 FOLD LOWER SPECIFIC ACTIVITY IN THE HIBERNATING
 CC ISOFORM.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 CC DEHYDROGENASE FAMILY.
 DR InterPro: IPR000173; GAP_dhydrogenase.
 DR Pfam: PF00044; gpdh; 1.
 DR PROSITE: PS00071; GAPDH: PARTIAL.
 KM Glycolysis; Oxidoreductase; NAD; ADP-ribosylation.
 FT VARIANT 6 6 N->D (IN HIBERNATING ADULT LIVER
 FT NON_TER 25 25 ISOFORM).
 SQ SEQUENCE 25 AA; 2603 MW; 4FC96C356CE79F2D CRC64;

Query Match 22.2%; Score 22; DB 1; Length 25;
 Best Local Similarity 55.6%; Pred. No. 1.7e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 VEGHERMGR 10
 11:11:
 Db 5 VNGFRIGR 13

RESULT 16
 METE_CANAL STANDARD; PRT; 25 AA.
 ID METE_CANAL
 AC P82610;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase
 DE (EC 2.1.1.14) (Methionine synthase, vitamin-B12 independent isozyme)
 DE (Cobalamin-independent methionine synthase) (Fragments).
 GN MET6.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE OF 1-14.
 RC STRAIN=SC5314;
 RA Pitarich A., Diaz-Orejas R., Molero G., Pardo M., Sanchez M.,
 RA Nombela C., Gil C.;
 RT "A proteomic approach to analyse the serologic response to Candida
 RT albicans systemic infection in a murine model.";
 RL Submitted (JUN-2000) to the SWISS-PROT data bank.
 RN [2]
 RP SEQUENCE OF 15-25, AND MASS SPECTROMETRY.
 RC STRAIN=SC5314;
 RA MEDLINE=20403418; PubMed=10949142;
 RA Pardo M., Ward M., Pitarich A., Sanchez M., Nombela C., Blackstock W.,
 RA Gil C.;

RT "Cross-species identification of novel Candida albicans immunogenic
 RT proteins by combination of two-dimensional polyacrylamide gel
 RT electrophoresis and mass spectrometry.";
 RL Electrophoresis 21:2651-2659(2000).
 CC -1- FUNCTION: CATALYZES THE TRANSFER OF A METHYL GROUP FROM 5-
 CC METHYLTERAHYDROFOLATE TO HOMOCYSTEINE RESULTING IN METHIONINE
 CC FORMATION.
 CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-
 CC homocysteine = tetrahydropteroyltri-L-glutamate + L-methionine.
 CC -1- COFACTOR: ZINC (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE DE NOVO BIOSYNTHESIS OF METHIONINE.
 CC -1- SIMILARITY: BELONGS TO THE VITAMIN-B12 INDEPENDENT METHIONINE
 CC SYNTHASE FAMILY.
 DR COMPUYEAST-2DPAGE; P82610; -
 KM Transferase; Methyltransferase; Methionine biosynthesis; Zinc.
 FT NON_CONS 14 15

FT UNSURE 18 18 OR I.
 FT UNSURE 22 22 OR I.
 FT NON_TER 25 25
 SQ SEQUENCE 25 AA; 2710 MW; 9888B56C2352D81 CRC64;

Query Match 22.2%; Score 22; DB 1; Length 25;
 Best Local Similarity 35.3%; Pred. No. 1.7e+03;
 Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 NYPHERMGRRTSSKE 17
 : | | | : | | :
 Db 4 DVLEPFRIGXQTLTLE 20

RESULT 17
 ID IDBP4_PIG STANDARD; PRT; 16 AA.
 AC P24854;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 RT Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
 DE (IGF-binding protein 4) (fragment).
 GN IGFBP4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92109718; PubMed=1722398;
 RA Coleman M.E., Pan Y.-C.E., Eberhart T.D.;
 RT "Identification and NH2-terminal amino acid sequence of three
 insulin-like growth factor-binding proteins in porcine serum.";
 RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
 CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS
 AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
 PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE
 INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Secreted
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
 CC PROTEIN FAMILY.
 CC PIR: JH0517; JH0517.
 DR InterPro: IPR000867; Insl_gro_fac.pr.
 DR InterPro: IPR000716; Thyroglobulin.1.
 DR PROSITE: PS00222; IGF-BINDING; PARTIAL.
 DR PROSITE: PS00484; THYROGLOBULIN_1; PARTIAL.
 KM Growth factor binding.
 NT NON_TER 16
 SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 21.2%; Score 21; DB 1; Length 16;
 Best Local Similarity 37.5%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGHERMGR 10
 | | | : | :
 Db 9 PSEKRLAR 16

RESULT 18
 ID IDBP4_PIG STANDARD; PRT; 18 AA.
 AC P01206;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin beta (Beta-MSH).
 OS Scylliorhinus beta (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scylliorhinidae; Scylliorhinus.

OX NCBI_TaxID=7830;

RN [1]
 RP SEQUENCE.
 RX MEDLINE=75113445; PubMed=4452470;
 RA Love R.M., Pickering B.T.;
 RT "A beta-MSH in the pituitary gland of the spotted dogfish
 (Scylliorhinus beta): isolation and structure.";
 RL Gen. Comp. Endocrinol. 24:398-404(1974).
 CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
 DR PIR: A01470; MTDIBC.
 KW Hormone.
 SQ SEQUENCE 18 AA; 2195 MW; 353C93A30C314DF4 CRC64;

Query Match 21.2%; Score 21; DB 1; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GHERMG 9
 | | | : | :
 Db 8 GHRMG 13

RESULT 19
 ID IDBP4_PIG STANDARD; PRT; 20 AA.
 AC P80902;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pyruvate synthase subunit PORC (EC 1.2.7.1) (Pyruvate oxidoreductase
 gamma chain) (POR) (Pyruvic-ferredoxin oxidoreductase gamma subunit)
 DE (Fragment).
 GN PORC.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97261844; PubMed=9108258;
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
 RT "Structures and functions of four anaerobic 2-oxoacid oxidoreductases
 in Methanobacterium thermoautotrophicum.";
 RL Eur. J. Biochem. 244:862-868(1997).
 CC -1- FUNCTION: THE PH OPTIMUM IS PH 10.0 AND THE OPTIMAL TEMPERATURE
 CC IS 80 DEGREES CELSIUS.
 CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
 CC CoA + CO(2) + reduced ferredoxin.
 CC -1- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
 CC GAMMA CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
 KM Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
 NT NON_TER 20
 SQ SEQUENCE 20 AA; 2167 MW; 481532134D42F353 CRC64;

Query Match 21.2%; Score 21; DB 1; Length 20;
 Best Local Similarity 28.6%; Pred. No. 1.9e+03;
 Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 HERMGRRTSSREL 18
 | | | : | :
 Db 7 HGRGQXAVTAIEI 20

RESULT 20
 ID IDBP4_PIG STANDARD; PRT; 25 AA.
 AC P20056;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuromedin U-25 (NmU-25).

OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine; PubMed=2592357;
RX MEDLINE=90078173; PubMed=2592357;
RA Domin J., Yiangou Y.G., Spokes R.A., Altken A., Parmar K.B.,
RT Chrysanthou B.U., Bloom S.R.,
RT "The distribution, purification, and pharmacological action of an
RT amphibian neuropeptide U."
RL J. Biol. Chem. 264:20881-20885(1989).
CC -1- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES
CC SELECTIVE VASOCONSTRICTION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NMU FAMILY.
DR PIR: A34179; A34179.
InterPro: IPR001942; NMU.
Pfam: PF02070; NMU; 1.
SMART: SMD0084; NMU; 1.
PROSITE: PS00967; NMU; 1.
KW Amidation; Hormone.
FT MOD_RES 25
SQ SEQUENCE 25 AA; 2832 MW; 6A01D89FDA06FD4 CRC64;
Query Match 21.2%; Score 21; DB 1; Length 25;
Best Local Similarity 35.7%; Pred. No. 2.4e+03;
Matches 5; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 3 PGHERMGRGRTSSK 16
DB 3 PDEELGPGGVLSR 16
RESULT 21
PGQ_XENLA
ID PGQ_XENLA STANDARD; PRT; 24 AA.
AC P39080;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE Antimicrobial peptide PGQ.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;
OC Xenopodidae; Xenopus.
NCBI_TaxID=8353;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=92011794; PubMed=1717472;
RA Moore K.S., Bevins C.L., Brasseur M.M., Tomassini N., Turner K.,
RA Eck H., Zasloff M.,
RT "Antimicrobial peptides in the stomach of Xenopus laevis."
RL J. Biol. Chem. 266:19851-19857(1991).
CC -1- FUNCTION: ANTIMICROBIAL PEPTIDE.
CC -1- TISSUE SPECIFICITY: IS SYNTHESIZED IN THE STOMACH AND STORED
CC IN A NOVEL GRANULAR MULTINUCLEATED CELL IN THE GASTRIC MUCOSA.
CC IT IS STORED AS ACTIVE, PROCESSED PEPTIDES IN LARGE GRANULES
CC WITHIN THE GRANULAR GLAND SECRETIONS OF THE SKIN.
CC -1- SIMILARITY: BELONGS TO THE MAGAININ FAMILY OF ANTIMICROBIAL
CC PEPTIDES.
DR PIR: A41037; A41037.
KW Antibiotic; Amphibian skin.
SQ SEQUENCE 24 AA; 2457 MW; 7E6A87CB7CF22B9C CRC64;
Query Match 20.7%; Score 20.5; DB 1; Length 24;
Best Local Similarity 41.7%; Pred. No. 2.8e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
QY 1 NVPGH-ERMGRG 11
DB 11:::11

DB 5 NVIGYKLKLTGTG 16
RESULT 22
CHOX_ALCSP
ID CHOX_ALCSP STANDARD; PRT; 7 AA.
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 01-APR-1990 (Rel. 14, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Eml S., Yamano T.,
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp."
RL J. Biochem. 88:197-203(1980).
CC -1- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR: A15398; A15398.
KW Oxidoreductase.
FT NON_TER 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;
Query Match 20.2%; Score 20; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 PGHER 7
DB 3 PNHSR 7
RESULT 23
PNOC_PIG
ID PNOC_PIG STANDARD; PRT; 17 AA.
AC P35791;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Nociceptin (Orphanin Fq).
GN PNOC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC TISSUE=Hypothalamus;
RX MEDLINE=96055113; PubMed=7481766;
RA Reinscheid R.K., Notthacker H.-P., Bourson A., Ardali A.,
RA Henningsen R.A., Bunzow J.R., Grandy D.K., Langen H., Monsma F.J., Jr.,
RA Civelli O.,
RT "Orphanin Fq, a neuropeptide that activates an opioidlike G protein-
RT coupled receptor."
RL Science 270:792-794(1995).
CC -1- FUNCTION: NOCICEPTIN IS THE LIGAND OF THE OPIOID RECEPTOR-LIKE
CC RECEPTOR (OPRL1). IT MAY ACT AS A TRANSMITTER IN THE BRAIN BY
CC MODULATING NOCICEPTIVE AND LOCOMOTOR BEHAVIOR. MAY BE INVOLVED IN
CC NEURONAL DIFFERENTIATION AND DEVELOPMENT. WHEN ADMINISTERED
CC INTRACEREBROVENTRICULARLY INTO MICE, THIS PEPTIDE INDUCES
CC HYPERALGESIA AND DECREASES LOCOMOTOR ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY IN THE BRAIN AND SPINAL CORD.
CC -1- SIMILARITY: BELONGS TO THE OPIOIDS NEuropeptides PRECURSORS
CC FAMILY.
DR InterPro: IPR000094; Opioid_neuropep.
DR PROSITE: PS01252; OPIOIDS_PRECURSOR; PARTIAL.
KW Opioid peptide; Neurotransmitter; Neuropeptide.

SQL	SEQUENCE	17 AA:	1809 MM:	3F63A785F8768409 CRC64:
	Query Match	20.2%;	Score 20;	DB 1; Length 17;
	Best Local Similarity	50.0%;	Pred. No. 2.4e+03;	
	Matches 4;	Conservative 3;	Mismatches 1;	Indels 0;
OY	12 RTSSKELA 19			
DB	8 RKSARKLA 15			
RESULT 24				
PK5__PERAM				
ID	PK5__PERAM	STANDARD:	PRT:	17 AA.
AC	P82617;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pyrokina-5 (pea-pk-5) (FXYRL-amide).			
OS	Periplaneta americana (American cockroach).			
CC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
CC	Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;			
CC	Blattoidea; Blattidae; Periplaneta.			
OX	NCBI_TaxID=6978;			
RN	[1]			
RP	SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.			
RC	TISSUE=Abdominal perisymphathetic organs;			
RC	MEDLINE=99212469; PubMed=10196736;			
RA	Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;			
RT	"Differential distribution of pyrokina-isoforms in cerebral and			
RT	abdominal neuromal organs of the American cockroach.";			
RT	Insect Biochem. Mol. Biol. 29:139-144(1999).			
RN	[2]			
RP	TISSUE SPECIFICITY.			
RC	MEDLINE=20189894; PubMed=10723010;			
RA	Predel R., Eckert M.;			
RT	"Tissue-specific distribution of EXPRlamides in the nervous system of			
RT	the American cockroach.";			
RC	J. Comp. Neurol. 419:352-363(2000).			
CC	-1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY			
CC	(MYOTROPIC ACTIVITY).			
CC	-1- TISSUE SPECIFICITY: MAINLY IN ABDOMINAL PERISYMPATHETIC ORGANS AND			
CC	TO A LESSER EXTENT IN RETROCEPHAL COMPLEX.			
CC	-1- MASS SPECTROMETRY: MW=1651.7; METHOD=MALDI.			
CC	-1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.			
DR	InterPro: IPR001484; Pyrokina.			
CC	PROSITE: PS00539; PYROKININ; 1.			
KW	Neuropeptide; Amidation; Pyrokina.			
RT	MOD_RES 17			
CC	SEQUENCE 17 AA: 1653 MW: 8527162EA45BBA54 CRC64:			
	Query Match	20.2%;	Score 20;	DB 1; Length 17;
	Best Local Similarity	66.7%;	Pred. No. 2.4e+03;	
	Matches 4;	Conservative 0;	Mismatches 2;	Indels 0;
OY	9 GGRGTS 14			
DB	4 GSGETS 9			
RESULT 25				
ID	TX3__PHONI	STANDARD:	PRT:	19 AA.
AC	P31010;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Neurotoxin Tx3 (Fragment).			
OS	Phenultria nigricauda (Brazilian armed spider).			
CC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;			
CC	Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phenultria.			
CC	NCBI_TaxID=6918;			
RN	[1]			

RP	SEQUENCE
RQ	TISSUE-Venom:
FX	MEDLINE=92196803; PubMed-1801316;
RA	"Resende L. Jr., Cordello M.N., Oliveira E.B., Diniz C.R.;
RT	"Isolation of neurotoxic peptides from the venom of the 'armed'
RL	spider Phoneutria nigriventer.";
CC	Toxicon 29:1225-1233(1991)."
CC	-I FUNCTION: ANTAGONIST OF L-TYPE CALCIUM CHANNELS (By similarity).
CC	-I SUBCELLULAR LOCATION: Secreted.
CC	-I SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY.
DR	PIR: G39305; G39305.
KW	Calcium channel inhibitor; Toxin; Neurotoxin.
FT	NON_TER 19
SQ	SEQUENCE 19 AA; 2244 MW; 321AE89CF10F7587 CRC64;
Query Match	20.2%; Score 20; DB 1; Length 19;
Best Local Similarity	30.0%; Pred. No. 2.7e+03;
Matches	3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY	8 MGRCRTSKSE 17 :: :: :: DB 3 IGRENESQRKD 12

Search completed: March 14, 2003, 16:06:07
Job time : 31 secs



GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:04:22 ; Search time 29 Seconds
(without alignments)
134.996 Million cell updates/sec

Title: US-09-674-913a-1
Perfect score: 99
Sequence: 1 NVPCHRMGRGRTSSKELA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 9297

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

SPTRMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_oraneller:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31.3	24	4	08RXU1	08rxu1 homo sapien
2	29.3	18	4	015912	015912 homo sapien
3	28.3	23	10	09M7J2	09m7j2 hordium chi
4	28.3	23	11	09K2R1	09k2r1 rattus norv
5	27.3	17	4	013376	013376 homo sapien
6	27.3	20	13	09DEH9	09deh9 xenopus lae
7	27.3	24	8	09GFA0	09gfa0 calycanthus
8	26.3	19	15	0905H2	0905h2 human immun
9	26.3	20	15	09DYR0	09dyr0 human immun
10	26.3	24	4	09R573	09r573 nitrosomona
11	26.3	24	4	09GCT8	09gct8 homo sapien
12	26.3	24	11	08VHY7	08vhy7 mus musculu
13	25.3	19	4	09R763	09r763 rhizobium l
14	25.3	19	4	016271	016271 homo sapien
15	25.3	19	12	085658	085658 reovirus (t
16	25.3	21	11	09QUZ0	09quz0 rattus sp.

17	25.3	21	13	09DD39	09dd39 nipponia ni
18	25.3	22	13	057692	057692 otis tarda.
19	25.3	25	10	099215	099215 triticum mo
20	24.2	16	4	09UD45	09ud45 homo sapien
21	24.2	16	11	09R009	09r009 rattus norv
22	24.2	17	5	09V973	09v973 drosophila
23	24.2	17	10	09AUB3	09aub3 arabidopsis
24	24.2	19	6	09TRK3	09trk3 bos taurus
25	24.2	19	15	09ORG1	09org1 human immun
26	24.2	20	10	08RW5	08rw5 arabidopsis
27	24.2	22	13	0919P3	0919p3 ara millitar
28	24.2	23	3	09A1L1	09a1l1 magnetospir
29	24.2	23	3	09UR71	09ur71 lentinula e
30	24.2	24	10	08RVD4	08rvd4 pinus sylve
31	24.2	25	8	09GCF2	09gcf2 dioscorea b
32	23.5	18	2	030888	030888 bradyrhizob
33	23.2	15	6	09R545	09r545 mycobacteri
34	23.2	15	6	09T0Q5	09t0q5 bos taurus
35	23.2	16	11	09QVA6	09qva6 mus sp. pro
36	23.2	18	2	09R501	09r501 bacillus su
37	23.2	20	1	09UWH0	09uwh0 thermococcu
38	23.2	20	11	09QU71	09qu71 rattus sp.
39	23.2	20	12	09ICE8	09ice8 tt virus. o
40	23.2	22	11	0922R6	0922r6 mus musculu
41	23.2	22	13	0918S8	0918s8 gallus gall
42	23.2	23	4	09UMI6	09umi6 homo sapien
43	23.2	23	4	09BYM6	09bym6 homo sapien
44	23.2	23	4	09EB48	09eb48 homo sapien
45	23.2	24	11	063983	063983 mus musculu
46	23.2	25	11	09QV57	09qv57 rattus norv
47	23.2	25	12	09J1H6	09j1h6 tt virus. o
48	23.2	25	12	09J1H4	09j1h4 tt virus. o
49	23.2	25	12	09J1G9	09j1g9 tt virus. o
50	23.2	25	12	09J1G7	09j1g7 tt virus. o
51	23.2	25	12	09J1E2	09j1e2 tt virus. o
52	23.2	25	12	09J1D8	09j1d8 tt virus. o
53	23.2	25	15	09WRP2	09wrp2 human immun
54	23.2	25	15	09W8V6	09w8v6 human immun
55	22.2	10	11	09QV57	09qv57 mus sp. pro
56	22.2	12	15	078845	078845 human immun
57	22.2	14	11	0920G5	0920g5 mus musculu
58	22.2	14	15	010229	010229 human immun
59	22.2	14	15	010230	010230 human immun
60	22.2	14	15	010235	010235 human immun
61	22.2	16	4	09BOP2	09bop2 homo sapien
62	22.2	19	12	09PKX2	09pkx2 tobacco vel
63	22.2	20	12	085617	085617 reovirus (t
64	22.2	21	10	041580	041580 triticum ae
65	22.2	21	13	P79889	P79889 gallus gall
66	22.2	21	15	087579	087579 chimpanzee
67	22.2	21	15	087581	087581 chimpanzee
68	22.2	22	6	09SKU7	09sku7 bos taurus
69	22.2	22	12	085664	085664 reovirus (t
70	22.2	23	1	09UWL2	09uwl2 pyrococcus
71	22.2	23	5	09Y002	09y002 melarhaphie
72	22.2	23	12	066204	066204 transmissib
73	22.2	23	12	066184	066184 porcine res
74	22.2	24	8	09JUN1	09jun1 neisseria m
75	22.2	24	16	09T158	09t158 angophora c
76	22.2	24	10	09S8Y5	09s8y5 colocasia e
77	22.2	25	2	09R4C8	09r4c8 mycoplasma
78	22.2	25	4	014497	014497 homo sapien
79	22.2	25	4	096OP2	096op2 homo sapien
80	22.2	25	5	023966	023966 dendrocoeli
81	22.2	25	15	09DUZ3	09duz3 human immun
82	22.2	25	15	071940	071940 human immun
83	22.2	25	15	071946	071946 human immun
84	22.2	25	15	091OP9	091op9 human immun
85	22.2	25	15	091O00	091o00 human immun
86	22.2	25	15	091O01	091o01 human immun
87	22.2	25	15	091O02	091o02 human immun
88	22.2	25	15	091O03	091o03 human immun
89	22.2	25	15	091O04	091o04 human immun

90	22	22.2	25	15	0910Q8	Q91qg8 human immun	163	20	20.2	18	11	062256	Q62256 mus musculus	
91	22	22.2	25	15	0910R0	Q91qr0 human immun	164	20	20.2	19	13	09PRU5	Q9PRU5 torpedo mar	
92	22	22.2	25	15	0910R1	Q91qr1 human immun	165	20	20.2	18	4	09UCC1	Q9UCC1 homo sapien	
93	22	22.2	25	15	0910R2	Q91qr2 human immun	166	20	20.2	19	10	09S8W0	Q9S8W0 triticum ae	
94	22	22.2	25	15	0910R3	Q91qr3 human immun	167	20	20.2	20	2	051558	051558 pseudomonas	
95	22	22.2	25	15	0910R4	Q91qr4 human immun	168	20	20.2	20	2	047598	047598 escherichia	
96	22	22.2	25	15	0910R5	Q91qr5 human immun	169	20	20.2	20	2	09S6C4	09S6C4 salmonella	
97	22	22.2	25	15	08QDX1	Q8qdx1 human immun	170	20	20.2	20	2	09R4H6	Q9R4H6 bacillus su	
98	22	22.2	25	15	08QDX7	Q8qdx7 human immun	171	20	20.2	20	5	09U8M6	Q9U8M6 liodrosophi	
99	21.5	21.7	20	2	09R551	Q9r551 bacillus me	172	20	20.2	20	11	09QV61	Q9QV61 rattus sp.	
100	21	21.2	11	12	08B616	Q8b616 avian infec	173	20	20.2	21	4	014595	014595 homo sapien	
101	21	21.2	11	15	09D232	Q9d232 human immun	174	20	20.2	21	5	025085	025085 herdamia m	
102	21	21.2	12	2	050303	050303 bacillus st	175	20	20.2	21	10	09S704	Q9S704 arabidopsis	
103	21	21.2	13	5	09W506	Q9W5q6 drosophila	176	20	20.2	21	15	09W7Z6	Q9W7Z6 human immun	
104	21	21.2	14	6	09N1V6	Q9n1v6 equus cabal	177	20	20.2	22	4	09UMG9	Q9UMG9 homo sapien	
105	21	21.2	15	1	09UMG1	Q9umg1 pyrococcus,	178	20	20.2	22	5	09BH35	Q9bh35 caenorhabdi	
106	21	21.2	15	10	09S8V6	Q9s8v6 triticum ae	179	20	20.2	22	13	013047	013047 xenopus lae	
107	21	21.2	16	4	09NY32	Q9ny32 homo sapien	180	20	20.2	23	4	016090	016090 homo sapien	
108	21	21.2	16	4	09GT79	Q9gt79 homo sapien	181	20	20.2	23	5	061341	061341 panullius l	
109	21	21.2	16	4	09UD46	Q9ud46 homo sapien	182	20	20.2	23	5	09TWE7	Q9twe7 pseudaletia	
110	21	21.2	16	6	09TRD1	Q9trd1 sus scrofa	183	20	20.2	23	6	09TRP7	Q9trp7 bos taurus	
111	21	21.2	16	10	082402	082402 fragaria nu	184	20	20.2	23	10	094IS9	Q94is9 pinus taeda	
112	21	21.2	16	10	082403	082403 fragaria ve	185	20	20.2	23	13	09PRV6	Q9prv6 anguilla ja	
113	21	21.2	16	10	082404	082404 fragaria ni	186	20	20.2	23	13	09PSA8	Q9psa8 xenopus bor	
114	21	21.2	16	10	082405	082405 fragaria li	187	20	20.2	23	15	08USK7	Q8usk7 human immun	
115	21	21.2	16	10	082406	082406 fragaria mo	188	20	20.2	24	2	09R7V0	Q9r7v0 streptococ	
116	21	21.2	16	10	082407	082407 fragaria vi	189	20	20.2	24	2	Q9R7V0	Q9r7v0 streptococ	
117	21	21.2	16	10	082781	Q82781 fragaria ve	190	20	20.2	24	5	P81594	P81594 desulfitoba	
118	21	21.2	17	8	036741	Q36741 homo sapien	191	20	20.2	24	5	P83215	P83215 octopus vul	
119	21	21.2	17	10	09S889	Q9s889 narcissus p	192	20	20.2	24	12	065700	065700 brome mosai	
120	21	21.2	18	2	09R583	Q9r583 aspergillus m	193	20	20.2	25	5	09BM65	Q9bm65 monostyla s	
121	21	21.2	18	3	002414	Q02414 aspergillus	194	20	20.2	25	6	09TR43	Q9tr43 bos taurus	
122	21	21.2	19	2	P74875	P74875 salmonella	195	20	20.2	25	6	09TR00	Q9tr00 sus scrofa	
123	21	21.2	19	4	09S578	Q9s578 homo sapien	196	20	20.2	25	10	094IS2	Q94is2 pinus radia	
124	21	21.2	19	4	09UCG2	Q9ucg2 homo sapien	197	20	20.2	25	11	09Q0Z6	Q9q0z6 mus sp. 205	
125	21	21.2	19	10	006914	Q06914 brassica na	198	20	20.2	25	12	09JIG2	Q9jig2 tt virus. o	
126	21	21.2	19	13	08UVE0	Q8uve0 gallus gall	199	20	20.2	25	12	09JIE5	Q9jie5 tt virus. o	
127	21	21.2	19	13	08UWH2	Q8uwh2 gallus gall	200	20	20.2	25	13	P83129	P83129 paratichthy	
128	21	21.2	20	4	Q9UD25	Q9ud25 homo sapien	201	20	20.2	25	15	09QEX7	Q9qex7 human immun	
129	21	21.2	20	11	Q9WPQ3	Q9wpq3 mus musculu	202	20	20.2	25	15	09W800	Q9w800 human immun	
130	21	21.2	20	13	Q9PMQ4	Q9pmq4 gallus gall	203	20	20.2	25	13	09PRV0	Q9prv0 anguilla ja	
131	21	21.2	22	4	09S597	Q9s597 homo sapien	204	20	20.2	25	10	086580	Q86580 simian para	
132	21	21.2	22	4	09BR41	Q9br41 homo sapien	205	20	20.2	26	4	09NY38	Q9ny38 homo sapien	
133	21	21.2	22	6	09NIF3	Q9nif3 gorilla gor	206	20	20.2	26	11	09TRW5	Q9trw5 bos taurus	
134	21	21.2	22	13	Q9PRN2	Q9prn2 petromyzon	207	20	20.2	26	11	09R0K9	Q9r0k9 mus musculu	
135	21	21.2	23	2	09LAB4	Q9lab4 rhodobacter	208	20	20.2	26	12	09TWY0	Q9twy0 fasciola he	
136	21	21.2	23	2	054449	Q54449 streptococ	209	20	20.2	26	12	13	08R2F6	Q8r2f6 rattus norv
137	21	21.2	23	8	035223	Q35223 oenothera b	210	20	20.2	26	12	11	09PS67	Q9ps67 gallus gall
138	21	21.2	24	4	016061	Q16061 homo sapien	211	20	20.2	26	13	4	09U0G9	Q9u0g9 homo sapien
139	21	21.2	24	11	088570	Q88570 mus musculu	212	20	20.2	26	13	5	09U5J3	Q9u5j3 trypanosoma
140	21	21.2	24	11	088571	Q88571 mus spretulu	213	20	20.2	26	14	4	09P2X4	Q9p2x4 homo sapien
141	21	21.2	25	2	047669	Q47669 escherichia	214	20	20.2	26	14	4	016484	Q16484 homo sapien
142	21	21.2	25	2	09R4N7	Q9r4n7 pseudomonas	215	20	20.2	26	15	2	09R546	Q9r546 mycobacteri
143	21	21.2	25	4	096HF0	Q96hf0 homo sapien	216	20	20.2	26	15	10	09AUA2	Q9aua2 maththiola i
144	21	21.2	25	5	023750	Q23750 ctenodrilus	217	20	20.2	26	15	11	0923G8	Q923g8 rattus norv
145	21	21.2	25	12	086949	Q86949 human herpe	218	20	20.2	26	16	4	096R75	Q96r75 homo sapien
146	21	21.2	25	12	086951	Q86951 human herpe	219	20	20.2	26	16	4	09UCW4	Q9ucw4 homo sapien
147	21	21.2	25	13	09PS48	Q9ps48 croctalus at	220	20	20.2	26	17	4	09HBD7	Q9hbd7 homo sapien
148	21	21.2	25	15	0910P8	Q91qp8 human immun	221	20	20.2	26	17	10	09AUA5	Q9aua5
149	20.5	20.7	25	12	091111	Q91i11 tt virus. o	222	20	20.2	26	17	11	09QV58	Q9qv58 mus sp. jac
150	20.5	20.7	25	12	0911D7	Q9j1d7 tt virus. o	223	20	20.2	26	18	3	096V21	Q96v21 cryptococcu
151	20.5	20.7	25	12	09U1D5	Q9u1d5 tt virus. o	224	20	20.2	26	18	7	077923	Q77923 oreochromis
152	20	20.2	10	11	09QV6E	Q9qv6e mus sp. pro	225	20	20.2	26	18	17	082TX6	Q82tx6 pyrobaculum
153	20	20.2	13	10	09X1W6	Q9x1w6 oryza sativ	226	20	20.2	26	19	2	09R4T9	Q9r4t9 bacillus th
154	20	20.2	14	2	P83077	P83077 bacillus ce	227	20	20.2	26	19	10	09S956	Q9s956 zea mays (m
155	20	20.2	15	3	P82468	P82468 pseudomonas	228	20	20.2	26	19	11	09QXp9	Q9qx9 mus musculu
156	20	20.2	15	3	Q96VH6	Q96vh6 penicillium	229	20	20.2	26	19	13	09PR59	Q9pr59 aeromonas h
157	20	20.2	15	12	Q66543	Q66543 human herpe	230	20	20.2	26	20	2	09KGR7	Q9kgr7 gallus gall
158	20	20.2	16	4	Q9NNZ2	Q9nnz2 homo sapien	231	20	20.2	26	20	4	08WVL1	Q8wvl1 homo sapien
159	20	20.2	17	4	Q91L80	Q91l80 enterococcu	232	20	20.2	26	20	4	09UCR9	Q9ucr9 homo sapien
160	20	20.2	17	6	09TQZ8	Q9tqz8 sus scrofa	233	20	20.2	26	20	4	09UCF1	Q9ucf1 homo sapien
161	20	20.2	18	6	09TR05	Q9tr05 bos taurus	234	20	20.2	26	20	4	09S8X5	Q9s8x5 glycine max
162	20	20.2	18	9	09XU05	Q9xu05 bacterioph	235	20	20.2	26	11	09QVF9	Q9qv9 rattus sp.	

236	19	19.2	20	11	09QVB2	09QVB2 mus sp. ser	309	19	19.2	25	15	071994	071994 human immun
237	19	19.2	20	11	09QVZ8	09QVZ8 rattus sp.	310	19	19.2	25	15	072001	072001 human immun
238	19	19.2	20	12	084861	084861 unidentified	311	19	19.2	25	15	072006	072006 human immun
239	19	19.2	21	2	051540	051540 pseudomonas	312	19	19.2	25	15	072016	072016 human immun
240	19	19.2	21	2	09R414	09R414 helicobacter	313	19	19.2	25	15	072020	072020 human immun
241	19	19.2	21	4	09H4Z8	09H4Z8 homo sapien	314	19	19.2	25	15	0910P7	0910P7 human immun
242	19	19.2	21	6	09GJX3	09GJX3 sus scrofa	315	19	19.2	25	15	0910Q7	0910Q7 human immun
243	19	19.2	21	7	09S554	09S554 mus muscullu	316	19	19.2	25	15	0910Q9	0910Q9 human immun
244	19	19.2	21	8	09TC76	09TC76 centropomus	317	18.5	18.7	21	5	024720	024720 drosophila
245	19	19.2	21	17	08RTG7	08RTG7 pyrococcus	318	18.5	18.7	25	5	09RW11	09RW11 aplysia cal
246	19	19.2	22	3	096V26	096V26 cryptococcu	319	18.5	18.7	25	11	P70382	P70382 mus muscullu
247	19	19.2	22	3	09UR51	09UR51 cryptococcu	320	18	18.2	8	2	056140	056140 streptococ
248	19	19.2	22	6	097568	097568 sus scrofa	321	18	18.2	10	2	P83067	P83067 bacillus ce
249	19	19.2	22	11	088449	088449 rattus norv	322	18	18.2	10	3	09UWV2	09UWV2 schizophyll
250	19	19.2	22	12	089826	089826 murine minu	323	18	18.2	10	10	P82937	P82937 hordium vul
251	19	19.2	23	2	09S6S7	09S6S7 rhodobacter	324	18	18.2	10	11	09QV66	09QV66 mus sp. pro
252	19	19.2	23	3	096V17	096V17 cryptococcu	325	18	18.2	11	5	P83321	P83321 penaeus mon
253	19	19.2	23	3	096V17	096V17 cryptococcu	326	18	18.2	11	5	099N81	099N81 mus muscullu
254	19	19.2	23	4	016209	016209 homo sapien	327	18	18.2	12	2	09R7F1	09R7F1 staphylococ
255	19	19.2	23	4	09BS58	09BS58 homo sapien	328	18	18.2	13	2	P94878	P94878 lactococcus
256	19	19.2	23	4	096155	096155 homo sapien	329	18	18.2	14	2	08VU21	08VU21 streptococ
257	19	19.2	23	5	09RWU5	09RWU5 trichoplusi	330	18	18.2	14	4	015222	015222 homo sapien
258	19	19.2	23	10	09S8Q6	09S8Q6 spinacia ol	331	18	18.2	15	4	09OC83	09OC83 homo sapien
259	19	19.2	23	11	09CT97	09CT97 mus muscullu	332	18	18.2	15	5	026323	026323 lymanea sta
260	19	19.2	23	11	061948	061948 mus muscullu	333	18	18.2	15	6	09YR89	09YR89 lymanea sta
261	19	19.2	23	11	08RO71	08RO71 mus muscullu	334	18	18.2	15	6	09YR45	09YR45 bos taurus
262	19	19.2	23	13	P70093	P70093 xenopus lae	335	18	18.2	15	9	09WMB7	09WMB7 vibrio phag
263	19	19.2	24	2	091720	091720 vibrio prot	336	18	18.2	15	10	P82430	P82430 nicotiana t
264	19	19.2	24	2	005124	005124 mycobacteri	337	18	18.2	15	11	09QVC4	09QVC4 rattus norv
265	19	19.2	24	2	09REB1	09REB1 escherichia	338	18	18.2	16	5	026322	026322 lymanea sta
266	19	19.2	24	2	09R4B2	09R4B2 streptococ	339	18	18.2	16	6	095M79	095M79 equus cabal
267	19	19.2	24	2	053923	053923 streptomyce	340	18	18.2	16	8	09Y2C2	09Y2C2 nicotiana t
268	19	19.2	24	5	09RTW6	09RTW6 trichoplusi	341	18	18.2	16	10	P93232	P93232 lycopersico
269	19	19.2	24	10	093776	093776 gossypium h	342	18	18.2	16	10	09S8D6	09S8D6 triticum ae
270	19	19.2	24	10	09S8U4	09S8U4 lycopersico	343	18	18.2	16	10	P82453	P82453 spinacia ol
271	19	19.2	24	11	09S8A6	09S8A6 secale cere	344	18	18.2	17	4	09EUB3	09EUB3 corynebacte
272	19	19.2	24	11	089021	089021 mus muscullu	345	18	18.2	17	4	016310	016310 homo sapien
273	19	19.2	24	11	09QV68	09QV68 rattus sp.	346	18	18.2	17	4	016073	016073 homo sapien
274	19	19.2	25	2	09WV14	09WV14 pseudomonas	347	18	18.2	17	10	09AUB2	09AUB2 arabis
275	19	19.2	25	2	09EYB8	09EYB8 escherichia	348	18	18.2	17	10	09AUB9	09AUB9 lepidium ca
276	19	19.2	25	4	09UCR8	09UCR8 homo sapien	349	18	18.2	17	11	08QV56	08QV56 mus sp. fkb
277	19	19.2	25	4	09UCN7	09UCN7 homo sapien	350	18	18.2	17	11	08QV56	08QV56 mus sp. fkb
278	19	19.2	25	5	09UIG8	09UIG8 euphorbia oc	351	18	18.2	18	6	095N16	095N16 sorex arane
279	19	19.2	25	5	08SZG6	08SZG6 drosophila	352	18	18.2	19	2	087732	087732 streptomyce
280	19	19.2	25	9	09ZMY2	09ZMY2 bacteriophag	353	18	18.2	19	2	005601	005601 pseudomonas
281	19	19.2	25	10	039914	039914 gossypium r	354	18	18.2	19	2	09R524	09R524 clostridium
282	19	19.2	25	10	039915	039915 gossypium r	355	18	18.2	19	3	09ETP8	09ETP8 cryptococcu
283	19	19.2	25	10	P81643	P81643 emilliana h	356	18	18.2	19	3	096TLL	096TLL cryptococcu
284	19	19.2	25	10	094199	094199 atropa bell	357	18	18.2	19	4	09UOG7	09UOG7 homo sapien
285	19	19.2	25	10	09S8V8	09S8V8 triticum ae	358	18	18.2	19	5	026321	026321 lymanea sta
286	19	19.2	25	11	063464	063464 rattus norv	359	18	18.2	19	6	09YR88	09YR88 canis famli
287	19	19.2	25	11	09QV18	09QV18 mus sp. glu	360	18	18.2	19	10	0947Y4	0947Y4 oryza sativ
288	19	19.2	25	11	09QV22	09QV22 mus sp. 10-	361	18	18.2	19	10	011358	011358 molluscum c
289	19	19.2	25	12	069148	069148 human herpe	362	18	18.2	19	12	090630	090630 baboon herp
290	19	19.2	25	13	091852	091852 xenopus lae	363	18	18.2	19	12	090633	090633 baboon herp
291	19	19.2	25	15	09DU42	09DU42 human immun	364	18	18.2	20	2	09R4O1	09R4O1 pseudomonas
292	19	19.2	25	15	099B06	099B06 human immun	365	18	18.2	20	3	096V30	096V30 cryptococcu
293	19	19.2	25	15	080273	080273 human immun	366	18	18.2	20	3	096V30	096V30 cryptococcu
294	19	19.2	25	15	071899	071899 human immun	367	18	18.2	20	3	012105	012105 rhizomucor
295	19	19.2	25	15	071906	071906 human immun	368	18	18.2	20	6	09YR88	09YR88 oryctolagus
296	19	19.2	25	15	071913	071913 human immun	369	18	18.2	20	6	09YR34	09YR34 ovis aries
297	19	19.2	25	15	071920	071920 human immun	370	18	18.2	20	6	09YR33	09YR33 canis famli
298	19	19.2	25	15	071927	071927 human immun	371	18	18.2	20	8	09RT14	09RT14 nicotiana s
299	19	19.2	25	15	071933	071933 human immun	372	18	18.2	20	10	P82163	P82163 spinacia ol
300	19	19.2	25	15	072010	072010 human immun	373	18	18.2	21	2	09X3C4	09X3C4 prochloroto
301	19	19.2	25	15	071876	071876 human immun	374	18	18.2	21	2	09R4D4	09R4D4 enterococcu
302	19	19.2	25	15	071882	071882 human immun	375	18	18.2	21	4	016218	016218 homo sapien
303	19	19.2	25	15	071887	071887 human immun	376	18	18.2	21	6	09YR45	09YR45 sus scrofa
304	19	19.2	25	15	071892	071892 human immun	377	18	18.2	21	13	09PS31	09PS31 elmeria ten
305	19	19.2	25	15	071969	071969 human immun	378	18	18.2	21	13	09PS31	09PS31 alligator m
306	19	19.2	25	15	071975	071975 human immun	379	18	18.2	22	2	034297	034297 agrobacteri
307	19	19.2	25	15	071981	071981 human immun	380	18	18.2	22	2	P82580	P82580 streptococ
308	19	19.2	25	15	071988	071988 human immun	381	18	18.2	22	3	096TLO	096TLO cryptococcu

382	18	18.2	22	4	Q96C75	Q96C75 homo sapien	455	18	18.2	25	2	Q9RAE3	Q9RAE3 escherichia
383	18	18.2	22	6	Q9TRY5	Q9TRY5 sus sp. ins	456	18	18.2	25	2	Q9R386	Q9R386 yersinia ps
384	18	18.2	22	8	Q9MSX9	Q9MSX9 arctium lap	457	18	18.2	25	3	Q96V10	Q96V10 cryptococcu
385	18	18.2	22	8	Q9MSX7	Q9MSX7 clisium vul	458	18	18.2	25	4	Q9UED3	Q9UED3 homo sapien
386	18	18.2	22	8	Q9MSX6	Q9MSX6 cousinia hy	459	18	18.2	25	7	Q19452	Q19452 mus sapien
387	18	18.2	22	8	Q9MSX4	Q9MSX4 cynara humi	460	18	18.2	25	8	Q9T213	Q9T213 mus musculu
388	18	18.2	22	8	Q9MSX3	Q9MSX3 echinops sp	461	18	18.2	25	8	Q9T213	Q9T213 nicotiana s
389	18	18.2	22	8	Q9MSX2	Q9MSX2 galactiles	462	18	18.2	25	12	Q9PX08	Q9PX08 foot-and-m
390	18	18.2	22	8	Q9MSX0	Q9MSX0 notobasis s	463	18	18.2	25	12	Q86944	Q86944 human herp
391	18	18.2	22	8	Q9MSW9	Q9MSW9 onopordum a	464	18	18.2	25	12	Q86945	Q86945 human herp
392	18	18.2	22	8	Q9MSW8	Q9MSW8 picnoman ac	465	18	18.2	25	12	Q86947	Q86947 human herp
393	18	18.2	22	8	Q9MSW6	Q9MSW6 silybum mar	466	18	18.2	25	15	Q9T006	Q9T006 human immun
394	18	18.2	22	8	Q9MSW5	Q9MSW5 tyrimus le	467	17.5	17.7	21	Q52033	Q52033 pseudomonas	
395	18	18.2	22	10	Q9XG00	Q9XG00 oryza sativ	468	17.5	17.7	21	Q924H1	Q924H1 mus muscul	
396	18	18.2	22	10	P81572	P81572 spinacia ol	469	17.5	17.7	23	Q9T2R3	Q9T2R3 solanum tub	
397	18	18.2	22	11	Q9S899	Q9S899 pinus monti	470	17	17.2	8	Q9L5W1	Q9L5W1 arabisidopsi	
398	18	18.2	22	11	Q9CVJ5	Q9CVJ5 mus muscul	471	17	17.2	9	Q9XSY1	Q9XSY1 canis fami	
399	18	18.2	22	16	Q9KAT7	Q9KAT7 bacillus ha	472	17	17.2	9	Q9H522	Q9H522 homo sapien	
400	18	18.2	23	2	Q9R4T0	Q9R4T0 bordetella	473	17	17.2	9	Q61723	Q61723 mus muscul	
401	18	18.2	23	2	Q9R570	Q9R570 nitrosomona	474	17	17.2	9	Q92766	Q92766 canine dist	
402	18	18.2	23	3	Q96TM9	Q96TM9 cryptococcu	475	17	17.2	11	Q9UR95	Q9UR95 pichia angu	
403	18	18.2	23	3	Q96TM8	Q96TM8 cryptococcu	476	17	17.2	11	Q60614	Q60614 homo sapien	
404	18	18.2	23	4	Q9UCR4	Q9UCR4 homo sapien	477	17	17.2	11	P82436	P82436 nicotiana t	
405	18	18.2	23	4	Q16312	Q16312 homo sapien	478	17	17.2	12	Q9L4M9	Q9L4M9 streptococ	
406	18	18.2	23	4	Q9UC00	Q9UC00 homo sapien	479	17	17.2	12	Q9TRT8	Q9TRT8 bos taurus	
407	18	18.2	23	4	Q9UC09	Q9UC09 homo sapien	480	17	17.2	12	Q9SYT4	Q9SYT4 arabisidopsi	
408	18	18.2	23	6	Q9TR07	Q9TR07 canis fami	481	17	17.2	12	Q61331	Q61331 mus muscul	
409	18	18.2	23	6	Q9MSX5	Q9MSX5 cynara card	482	17	17.2	13	Q9UCU2	Q9UCU2 homo sapien	
410	18	18.2	23	8	Q8SLH1	Q8SLH1 taraxacum (483	17	17.2	13	Q9T2U1	Q9T2U1 bos taurus	
411	18	18.2	23	8	Q8SLH0	Q8SLH0 taraxacum (484	17	17.2	14	Q56945	Q56945 yersinia ps	
412	18	18.2	23	12	Q84331	Q84331 simian virtu	485	17	17.2	14	P81715	P81715 streptomyc	
413	18	18.2	23	12	Q86946	Q86946 human herpe	486	17	17.2	14	Q9UCS5	Q9UCS5 homo sapien	
414	18	18.2	23	12	Q86948	Q86948 human herpe	487	17	17.2	14	Q9SAP8	Q9SAP8 pisum sativ	
415	18	18.2	23	12	Q9YYM1	Q9YYM1 border dise	488	17	17.2	14	P87540	P87540 barley mild	
416	18	18.2	23	12	Q9YYM0	Q9YYM0 border dise	489	17	17.2	14	P70007	P70007 xenopus lae	
417	18	18.2	23	12	Q9YYL9	Q9YYL9 border dise	490	17	17.2	14	Q10226	Q10226 human immun	
418	18	18.2	23	12	Q9YYL7	Q9YYL7 border dise	491	17	17.2	14	Q10227	Q10227 human immun	
419	18	18.2	23	12	Q9YYL6	Q9YYL6 border dise	492	17	17.2	14	Q10228	Q10228 human immun	
420	18	18.2	23	12	Q9YYL5	Q9YYL5 border dise	493	17	17.2	14	Q10232	Q10232 human immun	
421	18	18.2	23	12	Q9YYL4	Q9YYL4 border dise	494	17	17.2	14	Q10233	Q10233 human immun	
422	18	18.2	23	12	Q9YYL3	Q9YYL3 border dise	495	17	17.2	14	Q10234	Q10234 human immun	
423	18	18.2	23	12	Q9YYL2	Q9YYL2 border dise	496	17	17.2	15	Q9X635	Q9X635 escherichia	
424	18	18.2	23	12	Q9YYL1	Q9YYL1 border dise	497	17	17.2	15	Q9X637	Q9X637 klebsiella	
425	18	18.2	23	12	Q9YYL0	Q9YYL0 border dise	498	17	17.2	15	P83069	P83069 bacillus ce	
426	18	18.2	23	12	Q9YYK9	Q9YYK9 border dise	499	17	17.2	15	Q9Y429	Q9Y429 homo sapien	
427	18	18.2	23	12	Q9YYK8	Q9YYK8 border dise	500	17	17.2	15	Q9UEW3	Q9UEW3 homo sapien	
428	18	18.2	23	12	Q9YYK7	Q9YYK7 border dise	501	17	17.2	15	Q9UE41	Q9UE41 homo sapien	
429	18	18.2	23	13	Q13029	Q13029 boreogadus	502	17	17.2	15	Q9UCR5	Q9UCR5 homo sapien	
430	18	18.2	23	15	Q9EBS7	Q9EBS7 human immun	503	17	17.2	15	Q9TWS0	Q9TWS0 pyura stolo	
431	18	18.2	23	15	Q99DB8	Q99DB8 human immun	504	17	17.2	15	Q9TRP2	Q9TRP2 sus scrofa	
432	18	18.2	23	17	Q8Z2N4	Q8Z2N4 pyrobaculum	505	17	17.2	15	Q9TRN4	Q9TRN4 sus scrofa	
433	18	18.2	24	2	Q9EUI9	Q9EUI9 streptococ	506	17	17.2	15	Q9PRW3	Q9PRW3 crocalus at	
434	18	18.2	24	2	Q9KIL6	Q9KIL6 streptomyce	507	17	17.2	15	Q9PRM3	Q9PRM3 gallus gall	
435	18	18.2	24	2	Q9Z3Y9	Q9Z3Y9 pseudomonas	508	17	17.2	16	Q9UW44	Q9UW44 pyrococcus	
436	18	18.2	24	2	P81151	P81151 desulfovibrio	509	17	17.2	16	Q9LAP2	Q9LAP2 enterococcu	
437	18	18.2	24	4	Q9HB12	Q9HB12 homo sapien	510	17	17.2	16	Q9R5E4	Q9R5E4 aeromonas h	
438	18	18.2	24	5	Q26249	Q26249 drosophila	511	17	17.2	16	Q9RS56	Q9RS56 micrococcus	
439	18	18.2	24	5	Q44050	Q44050 trypanosoma	512	17	17.2	16	Q99374	Q99374 staphylococ	
440	18	18.2	24	5	Q24619	Q24619 drosophila	513	17	17.2	16	Q99898	Q99898 homo sapien	
441	18	18.2	24	8	Q9G0T1	Q9G0T1 rosa moscha	514	17	17.2	16	Q9TR09	Q9TR09 sus scrofa	
442	18	18.2	24	8	Q9G0T0	Q9G0T0 rosa phoeni	515	17	17.2	16	Q9TR75	Q9TR75 solanum tub	
443	18	18.2	24	8	Q9TIF2	Q9TIF2 lophostemon	516	17	17.2	16	Q9S6N2	Q9S6N2 nicotiana t	
444	18	18.2	24	8	Q9THL4	Q9THL4 myrtaceae g	517	17	17.2	16	Q54894	Q54894 mus muscul	
445	18	18.2	24	8	Q9TIF0	Q9TIF0 eucalyptops	518	17	17.2	16	Q9ERF8	Q9ERF8 ratius norv	
446	18	18.2	24	8	Q9TIF5	Q9TIF5 arillastrum	519	17	17.2	16	P90290	P90290 barley mild	
447	18	18.2	24	8	Q9TIF5	Q9TIF5 eucalyptus	520	17	17.2	17	Q9X515	Q9X515 enterococcu	
448	18	18.2	24	8	Q9TIF5	Q9TIF5 eucalyptus	521	17	17.2	17	Q8VME2	Q8VME2 pseudomonas	
449	18	18.2	24	8	Q9TIF5	Q9TIF5 eucalyptus	522	17	17.2	17	Q9RAV9	Q9RAV9 alcaligenes	
450	18	18.2	24	8	Q9GFW8	Q9GFW8 rosa gallic	523	17	17.2	17	Q9W421	Q9W421 enterococcu	
451	18	18.2	24	8	Q9GFW7	Q9GFW7 rosa hybrid	524	17	17.2	17	Q9W420	Q9W420 enterococcu	
452	18	18.2	24	8	Q9MSX8	Q9MSX8 carduus nut	525	17	17.2	17	Q18774	Q18774 crytocolagus	
453	18	18.2	25	2	Q45672	Q45672 bacillus su	526	17	17.2	17	Q9SK07	Q9SK07 sus scrofa	
454	18	18.2	25	2	Q9RAE2	Q9RAE2 escherichia	527	17	17.2	17	Q9TND0	Q9TND0 solanum tub	

528	17	17.2	17	11	0920M0	0920M0 rattus norv	601	17	17.2	21	2	09X3K5	09X3K5 prochloroco
529	17	17.2	17	15	0783J24	0783J24 human immun	602	17	17.2	21	2	09X3K9	09X3K9 prochloroco
530	17	17.2	17	15	0783J26	0783J26 human immun	603	17	17.2	21	2	09X3L4	09X3L4 prochloroco
531	17	17.2	18	2	09ZF30	09ZF30 salmonella	604	17	17.2	21	2	09WW38	09WW38 prochloroco
532	17	17.2	18	2	08RL15	08RL15 neisseria m	605	17	17.2	21	2	09WW38	09WW38 prochloroco
533	17	17.2	18	3	001672	001672 pneumocysti	606	17	17.2	21	2	09UR89	09UR89 prochloroco
534	17	17.2	18	4	09UE43	09UE43 homo sapien	607	17	17.2	21	6	09SKS4	09SKS4 ovis aries
535	17	17.2	18	4	09UC58	09UC58 homo sapien	608	17	17.2	21	6	09S7A0	09S7A0 sus scrofa
536	17	17.2	18	5	09TWE0	09TWE0 biophalari	609	17	17.2	21	6	09TRT1	09TRT1 sus taurus
537	17	17.2	18	10	09S892	09S892 glycine max	610	17	17.2	21	6	09TRR5	09TRR5 ovis aries
538	17	17.2	18	10	09S818	09S818 oryza sativ	611	17	17.2	21	6	09TRR1	09TRR1 ursus arcto
539	17	17.2	18	11	062532	062532 mus spreus	612	17	17.2	21	15	078504	078504 human immun
540	17	17.2	18	13	090791	090791 gallus gall	613	17	17.2	21	15	078484	078484 human immun
541	17	17.2	18	13	09PSR6	09PSR6 struthio ca	614	17	17.2	22	2	09F0R2	09F0R2 staphylococ
542	17	17.2	19	2	09S6B1	09S6B1 streptomyce	615	17	17.2	22	2	09ZF24	09ZF24 enterobacte
543	17	17.2	19	3	09UR87	09UR87 candida par	616	17	17.2	22	2	09ZAW2	09ZAW2 francisella
544	17	17.2	19	4	099711	099711 homo sapien	617	17	17.2	22	6	P81947	P81947 bos taurus
545	17	17.2	19	5	09N654	09N654 drosophila	618	17	17.2	22	8	09S7T4	09S7T4 abies alba
546	17	17.2	19	5	P82600	P82600 aedes aegyp	619	17	17.2	22	10	09S897	09S897 citrus sine
547	17	17.2	19	5	08TB86	08TB86 clona intes	620	17	17.2	22	11	09J1D6	09J1D6 mesocricetu
548	17	17.2	19	6	09BDD6	09BDD6 ovis aries	621	17	17.2	22	15	09Q6G8	09Q6G8 human immun
549	17	17.2	19	10	043370	043370 allium cepa	622	17	17.2	22	15	09Q6G2	09Q6G2 human immun
550	17	17.2	19	10	09JCN8	09JCN8 oryza sativ	623	17	17.2	22	15	09Q6G0	09Q6G0 human immun
551	17	17.2	19	10	P82245	P82245 splinacia ol	624	17	17.2	22	15	09Q6F6	09Q6F6 human immun
552	17	17.2	19	10	09S8W5	09S8W5 avena sativ	625	17	17.2	22	15	09Q6F2	09Q6F2 human immun
553	17	17.2	19	11	09JUK02	09JUK02 mus musculu	626	17	17.2	22	15	09Q6F0	09Q6F0 human immun
554	17	17.2	19	12	09JRK02	09JRK02 porcine cir	627	17	17.2	22	15	09Q6G8	09Q6G8 human immun
555	17	17.2	19	12	09YR03	09YR03 porcine cir	628	17	17.2	22	15	09Q6G6	09Q6G6 human immun
556	17	17.2	19	12	09YR05	09YR05 porcine cir	629	17	17.2	23	2	09S444	09S444 pseudomonas
557	17	17.2	19	12	09YR05	09YR05 porcine cir	630	17	17.2	23	2	09ZF27	09ZF27 klebsiella
558	17	17.2	19	12	091HA7	091HA7 porcine cir	631	17	17.2	23	4	09S2M2	09S2M2 enterococcu
559	17	17.2	19	13	056132	056132 porcine cir	632	17	17.2	23	4	09S2M7	09S2M7 enterococcu
560	17	17.2	19	15	09PRN4	09PRN4 petromyzon	633	17	17.2	23	4	09UC01	09UC01 homo sapien
561	17	17.2	20	2	09X629	09X629 human immun	634	17	17.2	23	5	09UC03	09UC03 homo sapien
562	17	17.2	20	2	09X630	09X630 unidentified	635	17	17.2	23	8	09S7T0	09S7T0 pinus sylve
563	17	17.2	20	2	09X632	09X632 leclercia a	636	17	17.2	23	8	09S7S8	09S7S8 secale cere
564	17	17.2	20	2	09X634	09X634 pseudomonas	637	17	17.2	23	10	09S8A3	09S8A3 rattus leuc
565	17	17.2	20	2	050089	050089 seirratia ma	638	17	17.2	23	11	062594	062594 cucumber mo
566	17	17.2	20	2	046499	046499 mycobacteri	639	17	17.2	23	12	089474	089474 cucumber mo
567	17	17.2	20	4	09WU7	09WU7 desulfivibr	640	17	17.2	23	12	089720	089720 cucumber mo
568	17	17.2	20	4	09NR04	09NR04 escherichia	641	17	17.2	23	12	06K265	06K265 cucurbit mo
569	17	17.2	20	4	09BRP3	09BRP3 homo sapien	642	17	17.2	23	13	09PRX7	09PRX7 xenopus lae
570	17	17.2	20	4	08WW61	08WW61 homo sapien	643	17	17.2	23	15	08S496	08S496 bovine leuk
571	17	17.2	20	4	09UCA0	09UCA0 homo sapien	644	17	17.2	24	2	09C630	09C630 streptococc
572	17	17.2	20	5	08WX06	08WX06 homo sapien	645	17	17.2	24	2	P94657	P94657 clostridium
573	17	17.2	20	5	09TWL2	09TWL2 octopus vul	646	17	17.2	24	2	09R2R0	09R2R0 streptococ
574	17	17.2	20	5	09UR85	09UR85 scapomyza	647	17	17.2	24	4	09UC38	09UC38 homo sapien
575	17	17.2	20	5	09UR82	09UR82 scapomyza	648	17	17.2	24	4	09UC21	09UC21 homo sapien
576	17	17.2	20	5	09UR89	09UR89 scapomyza	649	17	17.2	24	5	P91948	P91948 drosophila
577	17	17.2	20	6	028079	028079 bos taurus	650	17	17.2	24	6	046558	046558 sus scrofa
578	17	17.2	20	7	019685	019685 homo sapien	651	17	17.2	24	8	032057	032057 chlamydomon
579	17	17.2	20	11	09ET00	09ET00 mus musculu	652	17	17.2	24	10	096346	096346 brassica na
580	17	17.2	20	11	09OVH4	09OVH4 rattus sp.	653	17	17.2	24	10	09S806	09S806 triticum ae
581	17	17.2	20	11	09OUK8	09OUK8 rattus sp.	654	17	17.2	24	10	09S856	09S856 chlamydomon
582	17	17.2	20	11	09OUK8	09OUK8 rattus sp.	655	17	17.2	24	10	09S8B7	09S8B7 glycine max
583	17	17.2	20	11	08RAP6	08RAP6 mus musculu	656	17	17.2	24	11	09QVRL	09QVRL rattus sp.
584	17	17.2	20	11	08RLX7	08RLX7 mus musculu	657	17	17.2	25	1	09UMH1	09UMH1 pyrococcus
585	17	17.2	20	12	036978	036978 human papil	658	17	17.2	25	2	09X639	09X639 unidentified
586	17	17.2	20	12	08V9H3	08V9H3 chicken ane	659	17	17.2	25	2	09X641	09X641 citrobacter
587	17	17.2	20	12	08UXT4	08UXT4 hepatitis c	660	17	17.2	25	2	09X642	09X642 leclercia a
588	17	17.2	20	12	08UXT3	08UXT3 hepatitis c	661	17	17.2	25	2	09R5G2	09R5G2 lactobacilli
589	17	17.2	20	12	08UXT2	08UXT2 hepatitis c	662	17	17.2	25	3	09A149	09A149 saccharomyc
590	17	17.2	20	12	08UXT1	08UXT1 hepatitis c	663	17	17.2	25	4	09UOB1	09UOB1 homo sapien
591	17	17.2	20	12	08UXT0	08UXT0 hepatitis c	664	17	17.2	25	5	09BM01	09BM01 hydra litto
592	17	17.2	20	12	08UXS9	08UXS9 hepatitis c	665	17	17.2	25	5	09TWE4	09TWE4 drosophila
593	17	17.2	20	12	08UXS6	08UXS6 hepatitis c	666	17	17.2	25	5	09TXC6	09TXC6 asterias ru
594	17	17.2	20	12	08UXS5	08UXS5 hepatitis c	667	17	17.2	25	5	08T606	08T606 asterias ru
595	17	17.2	20	12	08UXS4	08UXS4 hepatitis c	668	17	17.2	25	6	09RLI4	09RLI4 sus scrofa
596	17	17.2	20	12	08UXS3	08UXS3 hepatitis c	669	17	17.2	25	10	040354	040354 medicago sa
597	17	17.2	20	12	08UXS2	08UXS2 hepatitis c	670	17	17.2	25	10	09S8M5	09S8M5 triticum ae
598	17	17.2	20	12	08UXS1	08UXS1 hepatitis c	671	17	17.2	25	12	037186	037186 hepatitis c
599	17	17.2	20	12	09PXE4	09PXE4 foot-and-mo	672	17	17.2	25	12	067095	067095 influenza vi
600	17	17.2	21	2	09X3F7	09X3F7 prochloroco	673	17	17.2	25	12	067095	067095 influenza vi

674	17	17.2	25	12	Q86943	Q86943 human herpe	747	16	16.2	17	12	Q85719	Q85719 reovirus (t
675	17	17.2	25	12	Q91061	Q91061 influenza a	748	16	16.2	17	12	Q919B0	Q919B0 human papil
676	17	17.2	25	12	Q91059	Q91059 influenza a	749	16	16.2	17	13	Q9DFR5	Q9DFR5 brachydanio
677	17	17.2	25	13	Q9YH56	Q9YH56 colurnix co	750	16	16.2	17	15	Q78328	Q78328 human immun
678	17	17.2	25	15	Q9WRES	Q9WRES human immun	751	16	16.2	17	15	Q78345	Q78345 human immun
679	17	17.2	25	15	Q80E38	Q80E38 human immun	752	16	16.2	17	16	Q9K704	Q9K704 bacillus ha
680	17	17.2	25	15	Q80E33	Q80E33 human immun	753	16	16.2	18	2	Q9R584	Q9R584 rhodobacter
681	17	17.2	25	15	Q80E27	Q80E27 human immun	754	16	16.2	18	4	Q9H113	Q9H113 homo sapien
682	17	17.2	25	15	Q80E21	Q80E21 human immun	755	16	16.2	18	4	Q14042	Q14042 homo sapien
683	16.5	16.7	25	2	Q9RBS9	Q9RBS9 pseudomonas	756	16	16.2	18	4	Q96F98	Q96F98 homo sapien
684	16	16.2	9	4	Q9UCQ9	Q9UCQ9 homo sapien	757	16	16.2	18	6	Q9GKH1	Q9GKH1 macaca mula
685	16	16.2	9	4	Q16220	Q16220 homo sapien	758	16	16.2	18	11	Q8VDM2	Q8VDM2 mus musculus
686	16	16.2	9	13	Q92009	Q92009 gallus gall	759	16	16.2	18	11	Q9IN55	Q9IN55 polymaviru
687	16	16.2	10	11	Q9QVF7	Q9QVF7 rattus sp.	760	16	16.2	18	12	Q919D5	Q919D5 human papil
688	16	16.2	11	5	P82698	P82698 leucophaea	761	16	16.2	18	12	Q919D3	Q919D3 human papil
689	16	16.2	11	7	Q77892	Q77892 oreochromis	762	16	16.2	18	12	Q919D1	Q919D1 human papil
690	16	16.2	11	7	Q77906	Q77906 oreochromis	763	16	16.2	18	12	Q919C9	Q919C9 human papil
691	16	16.2	11	7	Q77918	Q77918 pseudotroph	764	16	16.2	18	12	Q919C7	Q919C7 human papil
692	16	16.2	11	12	Q40974	Q40974 cauliflower	765	16	16.2	18	12	Q919C5	Q919C5 human papil
693	16	16.2	12	4	Q9UC29	Q9UC29 homo sapien	766	16	16.2	18	12	Q919B7	Q919B7 human papil
694	16	16.2	12	13	Q69232	Q69232 bovine herp	767	16	16.2	18	12	Q919B9	Q919B9 human papil
695	16	16.2	12	13	Q90213	Q90213 xenopus lae	768	16	16.2	18	12	Q919B7	Q919B7 human papil
696	16	16.2	13	2	Q9RF37	Q9RF37 actinobacil	769	16	16.2	18	12	Q919B5	Q919B5 human papil
697	16	16.2	13	2	Q936V1	Q936V1 pseudomonas	770	16	16.2	18	12	Q919B3	Q919B3 human papil
698	16	16.2	13	4	Q9NR93	Q9NR93 homo sapien	771	16	16.2	18	12	Q919A8	Q919A8 human papil
699	16	16.2	14	4	Q9NY40	Q9NY40 homo sapien	772	16	16.2	18	15	Q87589	Q87589 chimpanzee
700	16	16.2	14	4	Q96062	Q96062 homo sapien	773	16	16.2	18	15	Q87591	Q87591 chimpanzee
701	16	16.2	14	5	P82209	P82209 bombyx mori	774	16	16.2	18	15	Q87593	Q87593 chimpanzee
702	16	16.2	14	5	P82209	Q9FYF0 allium cepa	775	16	16.2	19	1	Q9WTR8	Q9WTR8 thermoplas
703	16	16.2	14	10	Q94IT6	Q94IT6 fragaria nu	776	16	16.2	19	2	Q9R2F7	Q9R2F7 escherichia
704	16	16.2	14	10	P82327	P82327 pisum sativ	777	16	16.2	19	2	Q9R4B9	Q9R4B9 streptococ
705	16	16.2	14	11	Q61864	Q61864 mus musculu	778	16	16.2	19	2	Q9R5C8	Q9R5C8 pseudomonas
706	16	16.2	14	12	Q85662	Q85662 reovirus (t	779	16	16.2	19	2	Q9R4X3	Q9R4X3 bacillus ce
707	16	16.2	14	12	Q84708	Q84708 porcine epi	780	16	16.2	19	3	Q92321	Q92321 saccharomyc
708	16	16.2	14	15	Q10231	Q10231 human immun	781	16	16.2	19	4	Q95598	Q95598 homo sapien
709	16	16.2	15	2	Q9R544	Q9R544 mycobacteri	782	16	16.2	19	4	Q9UC11	Q9UC11 homo sapien
710	16	16.2	15	8	Q9T2H9	Q9T2H9 nicotiana s	783	16	16.2	19	4	Q9UDB7	Q9UDB7 homo sapien
711	16	16.2	15	9	Q38574	Q38574 bacterioph	784	16	16.2	19	5	Q9TWJ7	Q9TWJ7 mytilus edu
712	16	16.2	15	10	Q9S8Q8	Q9S8Q8 ricinus com	785	16	16.2	19	6	Q19107	Q19107 bos taurus
713	16	16.2	15	11	Q90XZ5	Q90XZ5 mus musculu	786	16	16.2	19	11	Q9S8G6	Q9S8G6 colocasia e
714	16	16.2	15	13	Q9PS10	Q9PS10 gallus gall	787	16	16.2	19	11	Q9C806	Q9C806 mus musculu
715	16	16.2	16	2	Q50900	Q50900 shigella so	788	16	16.2	19	12	Q86050	Q86050 human herpe
716	16	16.2	16	3	Q9UR86	Q9UR86 candida par	789	16	16.2	19	13	Q9D821	Q9D821 gallus gall
717	16	16.2	16	4	Q9UD47	Q9UD47 homo sapien	790	16	16.2	19	13	Q91433	Q91433 gallus gall
718	16	16.2	16	5	Q18378	Q18378 drosophila	791	16	16.2	19	13	Q42416	Q42416 gallus gall
719	16	16.2	16	6	Q77491	Q77491 nycticebus	792	16	16.2	19	13	Q91983	Q91983 gallus gall
720	16	16.2	16	6	Q9TRK9	Q9TRK9 canis famill	793	16	16.2	19	15	Q91N44	Q91N44 human immun
721	16	16.2	16	6	Q9T505	Q9T505 bos taurus	794	16	16.2	19	15	Q85728	Q85728 spleen necr
722	16	16.2	16	6	Q9TRJ5	Q9TRJ5 bos taurus	795	16	16.2	19	15	Q905K4	Q905K4 human immun
723	16	16.2	16	6	Q9TRH0	Q9TRH0 bos taurus	796	16	16.2	19	15	Q905K0	Q905K0 human immun
724	16	16.2	16	6	Q9T2Q4	Q9T2Q4 brassica na	797	16	16.2	19	15	Q905H6	Q905H6 human immun
725	16	16.2	16	8	Q8SL50	Q8SL50 aconitum mas	798	16	16.2	19	15	Q905G4	Q905G4 human immun
726	16	16.2	16	10	P83187	P83187 basella alb	799	16	16.2	20	1	Q9UWJ3	Q9UWJ3 pyrococcus
727	16	16.2	16	11	Q90UM5	Q90UM5 rattus sp.	800	16	16.2	20	2	Q9R896	Q9R896 chlamydia t
728	16	16.2	16	12	Q919C3	Q919C3 polymaviru	801	16	16.2	20	2	P72423	P72423 saccharopol
729	16	16.2	16	12	Q919C3	Q919C3 human papil	802	16	16.2	20	2	Q9R5R7	Q9R5R7 mycobacteri
730	16	16.2	17	13	Q9PSL6	Q9PSL6 gallus gall	803	16	16.2	20	2	Q9R5C0	Q9R5C0 streptomyc
731	16	16.2	17	1	Q9UWLP	Q9UWLP pyrococcus	804	16	16.2	20	2	Q9R4F4	Q9R4F4 aeromonas h
732	16	16.2	17	2	Q9ZG32	Q9ZG32 chlamydia t	805	16	16.2	20	2	Q9R4C7	Q9R4C7 mycobacteri
733	16	16.2	17	2	Q9R4H9	Q9R4H9 bordetella	806	16	16.2	20	2	Q9R4S0	Q9R4S0 mycobacteri
734	16	16.2	17	3	Q9C0S9	Q9C0S9 claviiceps p	807	16	16.2	20	2	Q9R4P2	Q9R4P2 brevundimon
735	16	16.2	17	3	Q9C0S8	Q9C0S8 claviiceps p	808	16	16.2	20	2	Q9R4U6	Q9R4U6 pseudomonas
736	16	16.2	17	3	Q9C0S7	Q9C0S7 claviiceps s	809	16	16.2	20	4	Q60696	Q60696 homo sapien
737	16	16.2	17	3	Q9C0S6	Q9C0S6 claviiceps a	810	16	16.2	20	4	Q9UC20	Q9UC20 homo sapien
738	16	16.2	17	3	Q9C108	Q9C108 claviiceps f	811	16	16.2	20	5	Q9U2M0	Q9U2M0 caenorhabd
739	16	16.2	17	3	Q96T04	Q96T04 diaporthie p	812	16	16.2	20	5	P82310	P82310 panulirus j
740	16	16.2	17	3	Q94758	Q94758 sclerotinia	813	16	16.2	20	6	Q9TRH7	Q9TRH7 canis famill
741	16	16.2	17	4	Q9UC89	Q9UC89 homo sapien	814	16	16.2	20	6	Q9TRR5	Q9TRR5 ovis aries
742	16	16.2	17	5	Q9TWP6	Q9TWP6 artemia (br	815	16	16.2	20	10	P83186	P83186 basella alb
743	16	16.2	17	6	Q9SM49	Q9SM49 bos taurus	816	16	16.2	20	10	Q9S900	Q9S900 vigna sinen
744	16	16.2	17	8	Q9T0Z5	Q9T0Z5 macaca fasc	817	16	16.2	20	10	Q9S8U6	Q9S8U6 triticum ae
745	16	16.2	17	8	Q9T579	Q9T579 pinelodella	818	16	16.2	20	10	Q9S8T1	Q9S8T1 trichosanthe
746	16	16.2	17	10	Q65345	Q65345 gossypium h	819	16	16.2	20	10	Q9S8H8	Q9S8H8 brassica na

820	16	16.2	20	11	090U8	09qu8 mus sp. c-m	893	16	16.2	24	8	037804	037804 iris chryso
821	16	16.2	20	13	09PRN3	09prn3 petromyzon	894	16	16.2	24	8	037829	037829 iris harte
822	16	16.2	20	13	09PS14	09ps14 oncorhynch	895	16	16.2	24	8	037824	037824 iris doula
823	16	16.2	21	2	09UP68	09up68 iacobacill	896	16	16.2	24	8	032467	032467 iris purdyi
824	16	16.2	21	3	09R5E0	09rte0 aeromonas h	897	16	16.2	24	8	032458	032458 iris innoti
825	16	16.2	21	3	09URT6	09ut6 schizosacch	898	16	16.2	24	10	039759	039759 gossypium a
826	16	16.2	21	4	015965	015965 homo sapien	899	16	16.2	24	10	P82139	P82139 spiniacia ol
827	16	16.2	21	4	0968P6	0968p6 homo sapien	900	16	16.2	24	10	042505	042505 gossypium a
828	16	16.2	21	4	09UC16	09uc16 homo sapien	901	16	16.2	24	10	039918	039918 gossypium r
829	16	16.2	21	6	09N0J5	09n0j5 saginus lm	902	16	16.2	24	10	09S8G5	09s8g5 oryza sativ
830	16	16.2	21	6	09R0C8	09rtc8 coriatermes	903	16	16.2	24	11	08R2H8	08r2h8 mus musculu
831	16	16.2	21	8	08SL63	08sl63 aeonium cas	904	16	16.2	24	13	09PS59	09ps59 gallus gall
832	16	16.2	21	8	08SL47	08sl47 aeonium per	905	16	16.2	24	15	073766	073766 human immu
833	16	16.2	21	9	064183	064183 bacterioph	906	16	16.2	24	16	09K8M1	09k8m1 bacillus ha
834	16	16.2	21	11	P70657	P70657 rattus sp.	907	16	16.2	25	5	09NBE2	09nbe2 chironomus
835	16	16.2	21	12	09UG23	09ug23 lt virus. o	908	16	16.2	25	9	09R2V2	09r2v2 bacterioph
836	16	16.2	21	12	09UG30	09ug30 lt virus. o	909	16	16.2	25	10	040971	040971 pinus radia
837	16	16.2	21	13	09PSR6	09psr6 gallus gall	910	16	16.2	25	10	09S8R4	09s8r4 nicotiana t
838	16	16.2	21	13	09PRO1	09prq1 oncorhynch	911	16	16.2	25	11	064135	064135 mus sp. cal
839	16	16.2	21	15	082392	082392 human t-cel	912	16	16.2	25	11	060839	060839 mus musculu
840	16	16.2	21	15	082410	082410 human t-cel	913	16	16.2	25	11	091XN8	091xn8 rattus norv
841	16	16.2	21	15	082411	082411 human t-cel	914	16	16.2	25	11	090V49	090v49 rattus sp.
842	16	16.2	21	15	082412	082412 human t-cel	915	16	16.2	25	11	064341	064341 mus musculu
843	16	16.2	21	16	031871	031871 bacillus su	916	16	16.2	25	12	011472	011472 hepatitis c
844	16	16.2	22	2	093A12	093a12 thioabacillu	917	16	16.2	25	13	P82875	P82875 rana clamat
845	16	16.2	22	4	08W08	08w08 saccharomyc	918	16	16.2	25	15	09DU36	09du36 human immu
846	16	16.2	22	4	08W08	08w08 homo sapien	919	16	16.2	25	15	09DU28	09du28 human immu
847	16	16.2	22	4	09B224	09b224 homo sapien	920	16	16.2	25	15	09DU17	09du17 human immu
848	16	16.2	22	6	09N1W5	09n1w5 equus caball	921	16	16.2	25	15	09SBT5	09sbt5 human immu
849	16	16.2	22	6	09TRB7	09trb7 bos taurus	922	16	16.2	25	15	09SB56	09sb56 human immu
850	16	16.2	22	8	037142	037142 artemia par	923	16	16.2	25	15	09B52	09b52 human immu
851	16	16.2	22	8	09T2K1	09t2k1 spiniacia ol	924	16	16.2	25	15	09B8R8	09b8r8 human immu
852	16	16.2	22	8	09T2H8	09t2h8 nicotiana t	925	16	16.2	25	15	09B8R3	09b8r3 human immu
853	16	16.2	22	10	09PPD9	09fpd9 hevea brasl	926	16	16.2	25	15	09B8R0	09b8r0 human immu
854	16	16.2	22	11	09QV15	09qv15 mus sp. syn	927	16	16.2	25	15	09B8B3	09b8b3 human immu
855	16	16.2	22	11	09QV59	09qv59 cavia (guin	928	16	16.2	25	15	09B8B0	09b8b0 human immu
856	16	16.2	22	11	08R487	08r487 rattus norv	929	16	16.2	25	15	09B8P7	09b8p7 human immu
857	16	16.2	22	12	084172	084172 orf virus.	930	16	16.2	25	15	09B8P3	09b8p3 human immu
858	16	16.2	22	12	064831	064831 human adeno	931	16	16.2	25	15	09B8N0	09b8n0 human immu
859	16	16.2	22	13	0910C6	0910c6 gallinula c	932	16	16.2	25	15	09B8M6	09b8m6 human immu
860	16	16.2	22	13	0902V4	0902v4 rallus liml	933	16	16.2	25	15	09B8L1	09b8l1 human immu
861	16	16.2	22	13	0902V3	0902v3 rallus long	934	16	16.2	25	15	09B8K7	09b8k7 human immu
862	16	16.2	22	13	0902V2	0902v2 sarothura	935	16	16.2	25	15	09B8I7	09b8i7 human immu
863	16	16.2	22	15	P89772	P89772 human immu	936	16	16.2	25	15	09B8I5	09b8i5 human immu
864	16	16.2	23	2	09S580	09s580 pseudomonas	937	16	16.2	25	15	0910O5	0910o5 human immu
865	16	16.2	23	2	086455	086455 pseudomonas	938	16	16.2	25	16	08X3Y0	08x3y0 escherichia
866	16	16.2	23	2	086987	086987 proteus mir	939	16	16.2	25	17	08ZYY5	08zyy5 pyrobaculum
867	16	16.2	23	2	054956	054956 spirulina p	940	15.5	15.7	20	4	09BMT8	09bmt8 homo sapien
868	16	16.2	23	2	051776	051776 escherichia	941	15.5	15.7	20	13	09PRV5	09prv5 xenopus lae
869	16	16.2	23	4	09UC22	09uc22 homo sapien	942	15.5	15.7	20	13	090759	090759 gallus gall
870	16	16.2	23	4	09UCB0	09ucb0 homo sapien	943	15	15.2	8	6	09GWM3	09gmh3 lagenorhyn
871	16	16.2	23	4	09H4H9	09h4h9 homo sapien	944	15	15.2	8	7	09S213	09s213 cryotolagus
872	16	16.2	23	5	094781	094781 trypanosoma	945	15	15.2	8	7	09S213	09s213 cryotolagus
873	16	16.2	23	8	09MSH2	09msh2 sphagnum ca	946	15	15.2	8	7	094VA0	094va0 varanus sem
874	16	16.2	23	8	09MSH1	09msh1 sphagnum hyp	947	15	15.2	8	11	060615	060615 mus musculu
875	16	16.2	23	10	09S893	09s893 arachis fyp	948	15	15.2	9	2	045852	045852 clostridium
876	16	16.2	23	15	08USM2	08usm2 human immu	949	15	15.2	9	4	09UKR6	09ukf6 homo sapien
877	16	16.2	23	16	024856	024856 helicobacte	950	15	15.2	9	4	09UC36	09uc36 homo sapien
878	16	16.2	24	2	09ZF21	09zf21 proteus vul	951	15	15.2	9	4	09BXL4	09bxl4 homo sapien
879	16	16.2	24	2	09R4H1	09r4h1 amycolatops	952	15	15.2	9	6	09GJY3	09gjl3 lagenorhyn
880	16	16.2	24	2	08RL36	08rl36 burkholderi	953	15	15.2	9	6	09GJY2	09gjl2 lagenorhyn
881	16	16.2	24	3	007140	007140 saccharomyc	954	15	15.2	9	6	09GJY1	09gjl1 lagenorhyn
882	16	16.2	24	4	09BUC0	09buc0 homo sapien	955	15	15.2	9	6	09TT77	09tt77 bos taurus
883	16	16.2	24	4	08WYB9	08wyb9 homo sapien	956	15	15.2	9	11	008979	008979 mus musculu
884	16	16.2	24	5	09BMT0	09bmt0 spongilla l	957	15	15.2	9	12	P90359	P90359 barley mild
885	16	16.2	24	5	P82204	P82204 bombyx mori	958	15	15.2	10	2	08RSU1	08rsul helicobacte
886	16	16.2	24	7	09S9J2	09s9j2 drosophila	959	15	15.2	10	5	026093	026093 pisaster oc
887	16	16.2	24	7	078181	078181 homo sapien	960	15	15.2	10	5	P82223	P82223 bombyx mori
888	16	16.2	24	8	032444	032444 iris bracte	961	15	15.2	10	11	P82224	P82224 bombyx mori
889	16	16.2	24	8	032452	032452 iris fernal	962	15	15.2	10	11	09QVY9	09qv9 mus sp. pro
890	16	16.2	24	8	032459	032459 iris macros	963	15	15.2	10	13	09QVY3	09qv3 gallus gall
891	16	16.2	24	8	032471	032471 iris tenuis	964	15	15.2	11	2	09L4F7	09l4f7 bacillus ce
892	16	16.2	24	8	037085	037085 iris tenax	965	15	15.2	11	4	09UCU4	09ucu4 homo sapien

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966 15 15.2 11 4 09UCU3 09uc3 homo sapien
967 15 15.2 11 5 09TWM2 09twm2 aplysia cal
968 15 15.2 11 5 026092 026092 plaster oc
969 15 15.2 11 11 09Z1H5 09z1h5 mus musculu
970 15 15.2 12 2 005328 005328 sphingomona
971 15 15.2 12 2 047251 047251 escherichia
972 15 15.2 12 2 09R5F7 09r5f7 helicobacte
973 15 15.2 12 2 09R5F5 09r5f5 helicobacte
974 15 15.2 12 4 013865 013865 homo sapien
975 15 15.2 12 4 026429 026429 drosophila
976 15 15.2 12 6 09X531 09x531 sus scrofa
977 15 15.2 12 8 08SL49 08sl49 aequium lan
978 15 15.2 12 8 08SL40 08sl40 aequium urb
979 15 15.2 13 4 09REI2 09rei2 acidiphiliu
980 15 15.2 13 4 09UPE7 09upe7 homo sapien
981 15 15.2 13 4 099931 099931 homo sapien
982 15 15.2 13 4 09UCS4 09ucs4 homo sapien
983 15 15.2 8 09T369 09t369 zea mays (m
984 15 15.2 13 13 065331 065331 autographa
985 15 15.2 13 13 083009 083009 lamna nasus
986 15 15.2 14 2 09R7M3 09r7m3 bacillus st
987 15 15.2 14 2 085576 085576 chlamydia t
988 15 15.2 14 2 046291 046291 canadian pe
989 15 15.2 14 2 056750 056750 western x p
990 15 15.2 14 6 009061 009061 bos taurus
991 15 15.2 14 8 09T2K7 09t2k7 chlamydomon
992 15 15.2 14 10 082322 082322 pisum sativ
993 15 15.2 14 10 0852V1 0852v1 zea mays (m
994 15 15.2 14 12 08982 08982 hepatitis 9
995 15 15.2 14 12 09PY99 09py99 murine hepa
996 15 15.2 15 2 09R4D6 09r4d6 escherichia
997 15 15.2 15 2 09R547 09r547 mycobacteri
998 15 15.2 15 2 09R534 09r534 pseudomonas
999 15 15.2 15 2 09R5A1 09r5a1 micrococcus
1000 15 15.2 15 4 09UT51 09ut51 homo sapien
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ALIGNMENTS

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RESULT 1
08MXU1 PRELIMINARY: PRT: 24 AA.
AC 08MXU1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
BCL2-associated x protein (Fragment).
BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RA Thonborrow E.C., Schwartzfarb E.M., Manfredi J.J.;
RT "A conserved intronic response element mediates direct p53-dependent
transcriptional activation of both the human and murine bax genes.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF339054; AAL73333.1; -.
DR NON_TER
FT SEQUENCE 24 AA; 2379 MW; 8C3D3EB7479B798 CRC64;
SO Query Match 31.3%; Score 31; DB 4; Length 24;
Best Local Similarity 40.0%; Pred. No. 3e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

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OY 4 GHRMGRGRTSSKEL 18
Db 5 GROPGGGGTSSBOI 19
RESULT 2
```

```
015912
ID 015912 PRELIMINARY: PRT: 18 AA.
AC 015912;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Zinc finger homeodomain protein (Fragment).
GN ATBF1-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RA TISSUE=LUNG;
RX MEDLINE=96070776; PubMed=7592926;
RA Miura Y., Tam T., Ido A., Morinaga T., Miki T., Hashimoto T.,
RA Tamaoki T.;
RT "Cloning and characterization of an ATBF1 isoform that expresses in a
neuronal differentiation-dependent manner.";
RL J. Biol. Chem. 270:26840-26848(1995).
DR EMBL; L32833; AAC37582.1; -.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER
SO SEQUENCE 18 AA; 1960 MW; 5176F62C445BE7DE CRC64;
Query Match 29.3%; Score 29; DB 4; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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OY 7 RMGRGRTSSKEL 18
Db 2 RLGGGGQLVSEEL 13
RESULT 3
09W7J2 PRELIMINARY: PRT: 23 AA.
ID 09W7J2;
AC 09W7J2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE TAMADS 51-like protein (Fragment).
OS Hordeum chilense x Triticum durum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum x Triticum.
OX NCBI_TaxID=49967;
[1]
RN SEQUENCE FROM N.A.
RA STRAIN=HT174;
RA Salgueiro S., Gil J., Steele S.H., Savazzini F., Riley A.,
RA Lazzeri P.A., Barcelo P.;
RT "Sequence of part of a cereal MADS-box gene promoter.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF132736; AAP29592.1; -.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PSS0066; MADS_BOX_2; 1.
FT NON_TER
FT SEQUENCE 23 AA; 2723 MW; 7499F79B5D424418 CRC64;
SO Query Match 28.3%; Score 28; DB 10; Length 23;
Best Local Similarity 45.5%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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```
OY 8 MGRGRTSSKEL 18
Db 1 MGRCKIEIKRI 11
RESULT 4
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O922R1 ID Q922R1 PRELIMINARY; PRT; 23 AA.
AC Q922R1;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Histone H2A (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi Y.C.;
RT "DNA hypomethylation and germ cell-specific expression of testis-
specific H2B histone gene.";
RL Theis (1992), University of North Carolina at Chapel Hill.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9452395; PubMed=10524764;
RA Choi Y.C., Chae C.B.;
RT "The genomic and sequence analysis of rat histone H2B genes.";
RL DNA Seq. 9:353-358(1998).
DR EMBL: AF032898; AAC98916.1;
FT NON_TER 23
SQ SEQUENCE 23 AA; 2417 MW; CBEFFC323632794E CRC64;

Query Match 28.3%; Score 28; DB 11; Length 23;
Best Local Similarity 38.5%; Pred. No. 9.3e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 4 GHERMGRGRTSSK 16
DB 8 GCKRRRAKATSSR 20

RESULT 5
O13376 ID Q13376 PRELIMINARY; PRT; 17 AA.
AC Q13376;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RNA binding motif (Fragment).
GN RBM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97022533; PubMed=8875892;
RA Prosser J., Inglis J.D., Condie A., Ma K., Kerr S., Thakrar R.,
RA Taylor K., Cameron J.M., Cooke H.J.;
RT "Degeneracy in human multicopy RBM (YRRM), a candidate spermatogenesis
gene.";
RL Mamm. Genome 7:835-842(1996).
DR EMBL: U38450; AAB49815.1;
FT NON_TER 1
SQ SEQUENCE 17 AA; 2060 MW; 98CDD6AEFFC350012 CRC64;

Query Match 27.3%; Score 27; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 GGRGTS 14
DB 3 GGRGSS 8

RESULT 6
O9DEH9 ID Q9DEH9 PRELIMINARY; PRT; 20 AA.

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AC Q9DEH9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MCM4 (Fragment).
GN MCM4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J; TISSUE=SPLEEN;
RX MEDLINE=20456723; PubMed=11003390;
RA Fujimori A., Ataki R., Fukumura R., Ohnata T., Takahashi H.,
RA Kawahara A., Tatsumi K., Abe M.;
RT "Identification of four highly conserved regions in DNA-PKcs.";
RL Immunogenetics 51:965-973(2000).
DR EMBL: AB016729; BAB19264.1;
FT NON_TER 20
SQ SEQUENCE 20 AA; 2247 MW; 7F3A0A50B30441AB CRC64;

Query Match 27.3%; Score 27; DB 13; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 NYPGHERMGRGRTS 14
DB 6 STPSRRNRKRGKS 19

RESULT 7
O9GFA0 ID Q9GFA0 PRELIMINARY; PRT; 24 AA.
AC Q9GFA0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Photosystem II subunit (Fragment).
GN PSBH.
OS Calycanthus floridus (Sweet shrub).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Calycanthaceae; Calycanthus.
OX NCBI_TaxID=3429;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11080123;
RA Graham S.W., Olmstead R.G.;
RT "Utility of 17 chloroplast genes for inferring the phylogeny of the
RT basal angiosperms.";
RL Am. J. Bot. 87:1712-1730(2000).
DR EMBL: AF123846; AAG26264.1;
FT NON_TER 24
SQ SEQUENCE 24 AA; 2562 MW; F04BAD0139E57A11 CRC64;

Query Match 27.3%; Score 27; DB 8; Length 24;
Best Local Similarity 41.2%; Pred. No. 1.4e+03;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 2 VPGHERMGRGRTSSKEL 18
DB 6 VEGSSRSRGPRRTLTGDL 22

RESULT 8
O905H2 ID Q905H2 PRELIMINARY; PRT; 19 AA.
AC Q905H2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

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DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Fat protein (Fragment).
 OS Human immunodeficiency virus type 1
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-97CG275;
 RA Taniguchi Y., Takensia J., Bikandou B., Mboudjeka I.,
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
 RA Ichimura H., Parra H.-J.;
 RT "Genetic Subtypes of HIV Type 1 Based on the vif/vif Sequences in
 RT Republic of Congo-Brazzaville";
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF410446; AAL10250.1;
 FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA: 2290 MW: 366296E191128236 CRC64;

Query Match 26.3%; Score 26; DB 15; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.7e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 RMGRGRTSSKE 17
 DB 1 RGRGRTSSKE 11

RESULT 9
 GDBYR0 PRELIMINARY; PRT; 20 AA.
 ID Q9DYR0:
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE Gag polyprotein (Fragment).
 GN Gag.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20461476; PubMed=11005867;
 RA Martinez-Picado J., Depasquale M.P., Kartsonis N., Hanna G.J.,
 RA Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
 RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
 RA Siliciano R., D'Aquila R.T.;
 RT "Antiretroviral resistance during successful therapy of HIV type 1
 RT infection";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
 DR EMBL: AF292884; AAG25530.1;
 KW POLYPROTEIN.
 FT NON_TER 1 1
 SQ SEQUENCE 20 AA: 2436 MW: CODEC0F60B8539F CRC64;

Query Match 26.3%; Score 26; DB 15; Length 20;
 Best Local Similarity 45.5%; Pred. No. 1.8e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 MGRGRTSSKE 18
 DB 9 MWRGRTSSKE 19

RESULT 10
 Q9R573 PRELIMINARY; PRT; 24 AA.
 ID Q9R573:
 AC Q9R573;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE Hydroxylamine oxidoreductase (Fragment).
 OS Nitrosomonas europaea.

OC Bacteria; Proteobacteria; beta subdivision;
 OC Ammonia-oxidizing bacteria; Nitrosomonas.
 OX NCBI_TaxID=915;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=93315429; PubMed=8325841;
 RA Arciero D.M., Hooper A.B.;
 RT "Hydroxylamine oxidoreductase from Nitrosomonas europaea is a multimer
 RT of an octa-heme subunit";
 RL J. Biol. Chem. 268:14645-14654(1993).
 DR HSSP: 050925; IJGJ.
 SQ SEQUENCE 24 AA: 2663 MW: 7EC6594C5DC09D64 CRC64;

Query Match 26.3%; Score 26; DB 2; Length 24;
 Best Local Similarity 36.4%; Pred. No. 2.1e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 RMGRGRTSSKE 17
 DB 14 KIDRGRTSSKE 24

RESULT 11
 Q96GT8 PRELIMINARY; PRT; 24 AA.
 ID Q96GT8:
 AC Q96GT8;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Unknown (protein for IMAGe:4025108) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC009233; AAH09233.1;
 FT NON_TER 1 1
 SQ SEQUENCE 24 AA: 2698 MW: 1870BF6BA387E7A CRC64;

Query Match 26.3%; Score 26; DB 4; Length 24;
 Best Local Similarity 62.5%; Pred. No. 2.1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 GRTSSKE 18
 DB 11 GRPASREL 18

RESULT 12
 Q8VHY7 PRELIMINARY; PRT; 24 AA.
 ID Q8VHY7:
 AC Q8VHY7;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Bcl2-associated X protein (Fragment).
 GN BAX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Thompson E.C., Schwartz E.M., Manfredi J.J.;
 RT "A conserved intronic response element mediates direct p53-dependent
 RT transcriptional activation of both the human and murine bax genes";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF339055; AAL73334.1;

FT NON_TER 24 24
SQ SEQUENCE 24 AA: 2326 MW: 998C7EBB7479A6CC CRC64;

Query Match 26.3%; Score 26; DB 11; Length 24;
Best Local Similarity 41.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 6 ERMGRGRTSSKE 17
Db 6 EQLSGCGTSSSE 17

RESULT 13

ID 09R763 PRELIMINARY; PRT: 19 AA.
AC 09R763;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cpn60-1 protein (Fragment).

OS Rhizobium leguminosarum (biovar viciae).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=387;
RN [1]
RP SEQUENCE FROM N.A.

RC Wallington E.J., Smart D., Downie J.A., Lund P.A.;
RT "Distinct modes of regulation in two of the three chaperonin operons
of Rhizobium leguminosarum."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y12483; CAA73087.1; -.

FT NON_TER 19
SQ SEQUENCE 19 AA: 2196 MW: B046232A25C67C41 CRC64;

Query Match 25.3%; Score 25; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 CHERMGRC 11
Db 12 GREKMLRG 19

RESULT 14

ID 016271 PRELIMINARY; PRT: 19 AA.
AC 016271;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Arginine vasopressin V2 receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE-95086168; PubMed-7993996;
RA Holtzman E.J., Kolakowski L.F.Jr., Gelfman-Holtzman O., O'Brien D.G.,
RA Rasoulypour M., Guillot A.P., Ausiello D.A.;
RT "Mutations in the vasopressin V2 receptor gene in two families with
nephrogenic diabetes insipidus".
RL J. Am. Soc. Nephrol. 5:165-176(1994).
DR EMBL: S75754; AAB32753.1; -.

KW Receptor.
FT NON_TER 1
SQ SEQUENCE 19 AA: 1905 MW: 181640EFD90F2788 CRC64;

Query Match 25.3%; Score 25; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPCH 5
Db 1 VPCH 4

RESULT 15

ID 085658 PRELIMINARY; PRT: 19 AA.
AC 085658;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Reovirus serotype 2 L3 (Fragment).
OS Reovirus (type 2 / strain D5/Jones).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10865;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE-83017877; PubMed-7123853;
RA Galliard R.K., Li J.K., Keene J.D., Joklik W.K.;
RT "The sequences at the termini of four genes of the three reovirus
serotypes".
RL Virology 121:320-326(1982).
DR EMBL: J02305; AAA47244.1; -.

FT NON_TER 19
SQ SEQUENCE 19 AA: 2103 MW: D61D8C331FD8BAEF CRC64;

Query Match 25.3%; Score 25; DB 12; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 RMGRGRTSSK 16
Db 6 KRTGKSSGK 15

RESULT 16

ID 090UZO PRELIMINARY; PRT: 21 AA.
AC 090UZO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Alpha class glutathione S-transferase subunit 8 (EC 2.5.1.18)
(Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE-96036981; PubMed-7485987;
RA Rouimi P., Debrauner L., Tuillier J.;
RT "Electrospray ionization-mass spectrometry as a tool for
characterization of glutathione S-transferase isozymes".
RL Anal. Biochem. 229:304-312(1995).
DR HSSP: P24472; IGUK.
SQ SEQUENCE 21 AA: 2675 MW: AEA8DA961F24972C CRC64;

Query Match 25.3%; Score 25; DB 11; Length 21;
Best Local Similarity 71.4%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 9 GRGRTSS 15
Db 12 GRGRMES 18

RESULT 17

ID 09DD39 PRELIMINARY; PRT: 21 AA.
AC 09DD39;

DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Non-W chromodomain helicase DNA binding protein (W-linked chromodomain
helicase DNA binding protein) (Fragment).
GN NON-W CHD OR W-LINKED CHD.
OS Nipponia nippon.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Ciconiiformes; Threskiornithidae;
OC Nipponia.
OX NCBI_TaxID=128390;
RN [1]
RP SEQUENCE FROM N.A.
RA Arai Y., Ishii S., Kikuchi M.;
RT "Nipponia nippon non-W CHD gene."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Arai Y., Ishii S., Kikuchi M.;
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049444; BAB15805.1; -;
DR EMBL; AB049443; BAB15804.1; -;
KW Helicase.
FT NON_TER 1 1
FT 21 21
SQ SEQUENCE 21 AA; 2588 MW; C8E13B3B1AD353E3 CRC64;
Query Match 25.3%; Score 25; DB 13; Length 21;
Best Local Similarity 41.7%; Pred. No. 2.7e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 6 ERMGRGRTSSKE 17
Db 8 KKGRRPTPIPRE 19
RESULT 18
ID 057692 PRELIMINARY; PRT; 22 AA.
AC 057692;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CHROMO-helicase-DNA-binding ON A NON-W chromosome protein (Fragment).
GN CHD OR CHD-W.
OS Otis tarda.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruliformes; Otididae; Otis.
OX NCBI_TaxID=73107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-016, AND D16;
RA Pitra C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047391; AAC04869.1; -;
DR EMBL; AF047390; AAC04868.1; -;
KW DNA-binding; Helicase.
FT NON_TER 1 1
FT 22 22
SQ SEQUENCE 22 AA; 2675 MW; C8E13B3B1ABA5573 CRC64;
Query Match 25.3%; Score 25; DB 13; Length 22;
Best Local Similarity 41.7%; Pred. No. 2.9e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 6 ERMGRGRTSSKE 17
Db 9 KKGRRPTPIPRE 20
RESULT 19
Q99215
Q99215

ID Q99215 PRELIMINARY; PRT; 25 AA.
AC Q99215;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Albumin (Fragment).
OS Trilicium monococcum (Elkorn wheat) (Small spelt).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Trilicium.
OX NCBI_TaxID=4568;
RN [1]
RP SEQUENCE.
RA Shewry P.R., Lafandra D., Salcedo G., Aragoncillo C.;
RA Garcia-Olmedo F., Lew E.J.-L., Dietler M.D., Kasarda D.D.;
RL FEBS Lett. 175:359-363(1984).
DR HSSP; P01088; IIPA.
KW Seed storage protein.
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2585 MW; DA1FA028621066F0 CRC64;
Query Match 25.3%; Score 25; DB 10; Length 25;
Best Local Similarity 43.8%; Pred. No. 3.3e+03;
Matches 7; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 2 VPG---HERMGRGT 13
Db 7 VPGGLMPHPNPIGACRT 22
RESULT 20
ID Q9UD45 PRELIMINARY; PRT; 16 AA.
AC Q9UD45;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Gamma-interferon (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95038487; Pubmed=7951030;
RA Smirnova O.Iu., Tat'kov S.I., Petrenko V.A., Il'ichev A.A.,
RA Sandakhchiev L.S.;
RT "[Mutant human gamma-interferons with varied C-termini and their
properties].";
RL Dokl. Akad. Nauk 337:405-406(1994).
SQ SEQUENCE 16 AA; 2006 MW; 2CFED1938CCA84CB CRC64;
Query Match 24.2%; Score 24; DB 4; Length 16;
Best Local Similarity 45.5%; Pred. No. 3e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 6 ERMGRGRTSSK 16
Db 6 EMLFRGRRASQ 16
RESULT 21
ID Q9R0J9 PRELIMINARY; PRT; 16 AA.
AC Q9R0J9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Ras-GTPase-activating protein SH3-domain binding protein
(Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kitagawa Y., Nakamura K., Inoue K., Sakai T.;
 RT "Rat ras-GTPase-activating protein SH3-domain binding protein.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB032425; BAA84530.1;
 FT NON_TER
 SO SEQUENCE 16 AA; 1713 MW; 315DCEHC3BB10AB4 CRC64;
 Query Match 24.2%; Score 24; DB 11; Length 16;
 Best Local Similarity 40.0%; Pred. No. 3e+03;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Oy 8 MGRGRTSSKE 17
 Db 7 VGRGRTTPRO 16

RESULT 22

OX 09Y973 PRELIMINARY; PRT; 17 AA.
 AC 09Y973;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG12485 protein.
 GN CG12485.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Phrygotea; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 MD MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Zhang Q., Chen L.X.,
 RA Sutton R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fessler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jallali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry B., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003791; AAF57423.1;
 DR FLYBase; FBgn0034547; CG12485.
 SO SEQUENCE 17 AA; 1907 MW; 47D598D29F4860DE CRC64;

Query Match 24.2%; Score 24; DB 5; Length 17;
 Best Local Similarity 50.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 3 PGHERMGR 10
 Db 10 PHHAQOCR 17

RESULT 23

OX 09AUB3 PRELIMINARY; PRT; 17 AA.
 AC 09AUB3;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Chalcone synthase (Fragment).
 OS Arabidopsis thaliana subsp. halleri.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBI_TaxId=81971;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koch M., Kroymann J., Haubold B., Weisshaar B., Mitchell-Olds T.;
 RT "Phylogenetic analysis of promoter sequences from cruciferous
 RT plants";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF248986; AAK31921.1;
 FT NON_TER
 SO SEQUENCE 17 AA; 1752 MW; 31D56C76CB0E40CE CRC64;

Query Match 24.2%; Score 24; DB 10; Length 17;
 Best Local Similarity 45.5%; Pred. No. 3.2e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 8 MGRGRTSSKEL 18
 Db 3 MARGASSSDEI 13

RESULT 24

OX 09TRK3 PRELIMINARY; PRT; 19 AA.
 AC 09TRK3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE TCP-1 RING complex subunit P1 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCBI_TaxId=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93099850; PubMed=1361170;
 RA Frydman J., Nimmeggen E., Erdjument-Bromage H., Wall J.S., Tempst P.,
 RA Hartl F.U.;
 RT "Function in protein folding of Tric, a cytosolic ring complex
 RT containing TCP-1 and structurally related subunits.";
 RL EMBO J. 11:4767-4778(1992).
 DR InterPro: IPR002193; Chaperonin-TCP-1.
 DR InterPro: IPR002423; Cpn60/TCP-1.
 DR Pfam: PF00118; cpn60_TCP1; 1.
 DR PROSITE: PS00995; TCP1_3; 1.
 KW ATP-binding; Chaperone.

SQ SEQUENCE 19 AA; 1906 MW; 844291D811086990 CRC64;

Query Match

Best Local Similarity 24.2%; Score 24; DB 6; Length 19;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 6 ERMGRGRTSSKELA 19

Db 4 DEVGDGTTSTVTLA 17

RESULT 25

Q90RG1

ID Q90RG1 PRELIMINARY; PRT; 19 AA.

AC Q90RG1;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Tat protein (Fragment).

TAT.

OC Human immunodeficiency virus type 1.

OX Viruses; Retrovirdae; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=97CG257;

RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,

RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,

RA Hayami M., Ichimura H., Parra J.H.,

RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in

RT Republic of Congo-Brazzaville."

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF127549; AAK84910.1; -

FT NON_TER 1

FT NON_TER 1

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Search completed: March 14, 2003, 16:07:12

Up time : 53 secs

OY 7 RMGRGRTSSKE 17

Db 1 RQRRGTPSSRQ 11

Query Match 24.2%; Score 24; DB 15; Length 19;
Best Local Similarity 45.5%; Pred. No. 3.6e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:04:07 ; Search time 16 Seconds
(without alignments)
114.160 Million cell updates/sec

Title: US-09-674-913a-1
Perfect score: 99
Sequence: 1 NVPGERMGRGRTSSKELA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 4984

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: p1r73:*
2: p1r1:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	30.3	20	2	S48654
2	30	30.3	23	2	E39855
3	30	30.3	23	2	C39855
4	30	30.3	23	2	D39855
5	29	29.3	18	2	I53453
6	29	29.3	23	2	F39855
7	29	29.3	23	2	G39855
8	25	25.3	16	2	A31963
9	24	24.2	15	2	PL0143
10	24	24.2	16	2	PH0766
11	24	24.2	17	2	C30221
12	24	24.2	18	2	B24735
13	24	24.2	19	2	S28396
14	24	24.2	21	2	S29858
15	24	24.2	21	2	I50535
16	24	24.2	23	2	PC4030
17	24	24.2	24	2	S40666
18	23	23.7	16	2	S78415
19	23	23.2	15	2	JT0610
20	23	23.2	15	2	S36891
21	23	23.2	16	2	C45143
22	23	23.2	18	2	PS0387
23	23	23.2	22	2	I50533
24	23	23.2	23	2	I61239
25	23	23.2	24	2	I76886
26	22	22.2	13	2	S36668
27	22	22.2	16	2	H49037
28	22	22.2	17	2	A61334
29	22	22.2	20	2	E60894

30	22	22.2	21	2	B12055	glyceraldehyde-3-p
31	22	22.2	21	2	PT0227	Ig heavy chain CDK
32	22	22.2	21	2	C49042	Ig heavy chain V r
33	22	22.2	23	2	E54346	pyruvate synthase
34	22	22.2	23	2	S10448	nucleocapsid prote
35	22	22.2	23	2	G81890	hypothetical prote
36	22	22.2	23	2	S10609	dodecenoyl-CoA Del
37	22	22.2	25	2	A60842	somatostatin-25 -
38	21	21.2	11	2	PH0938	T-cell receptor be
39	21	21.2	12	2	PH0169	MAPK2 dehydrogenas
40	21	21.2	11	2	T44420	hypothetical prote
41	21	21.2	14	2	C33098	223K exoantigen -
42	21	21.2	15	2	A38304	heterogeneous ribo
43	21	21.2	16	2	C49039	T-cell receptor be
44	21	21.2	16	2	JH0517	Insulin-like growt
45	21	21.2	18	1	MTDEBC	melanotropin beta
46	21	21.2	19	2	S31613	beta-1,3-glucanase
47	21	21.2	20	2	S14161	probable drp-4-ke
48	21	21.2	20	2	S03505	T-cell receptor al
49	21	21.2	21	2	S69371	duodenase - bovine
50	21	21.2	21	2	A60975	HMG1/2 homolog - a
51	21	21.2	22	2	B60475	glyceraldehyde-3-p
52	21	21.2	22	2	PT0070	hypothetical prote
53	21	21.2	22	2	C42856	hypothetical prote
54	21	21.2	23	2	S43765	ribosomal protein
55	21	21.2	23	2	S16363	opacity protein P.
56	21	21.2	23	2	B30988	hypothetical prote
57	21	21.2	24	2	PN0163	glyceraldehyde-3-p
58	21	21.2	24	2	A60606	rhodopsin - Calfo
59	21	21.2	24	2	S53793	actin - mouse (fra
60	21	21.2	25	2	PC1119	atrolysin A (EC 3.
61	21	21.2	25	2	A34179	neurotrophin U - com
62	21	21.2	25	2	S39391	calpain II heavy c
63	20.5	20.7	24	2	A41037	antimicrobial pept
64	20	20.2	7	2	A15398	choline oxidase (E
65	20	20.2	15	2	S02381	probable membrane
66	20	20.2	15	2	PN0052	pyruvate kinase (E
67	20	20.2	16	2	PH1771	T cell receptor al
68	20	20.2	18	2	B27504	histone H2B - mous
69	20	20.2	18	2	A56676	hypothetical prote
70	20	20.2	19	2	S16332	peroxidase (EC 1.1
71	20	20.2	19	2	C39305	neurotoxin Tx3 - s
72	20	20.2	20	2	A05332	serum amyloid p-co
73	20	20.2	20	2	A47687	3-dehydroquinat d
74	20	20.2	20	2	S78759	ribosomal protein
75	20	20.2	21	2	S61410	pyruvate, phosphat
76	20	20.2	21	2	B49042	Ig heavy chain V r
77	20	20.2	22	2	A39269	LX-1 tumor antigen
78	20	20.2	23	2	A60423	monophenol monooxy
79	20	20.2	24	2	S59908	endothelial cell-v
80	20	20.2	25	2	S62673	glyceraldehyde-3-p
81	20	20.2	25	2	JP0047	ribosomal protein
82	20	20.2	25	2	JP0048	ribosomal protein
83	20	20.2	25	2	A35734	glial fibrillary a
84	19.5	19.7	18	2	S13974	chlorophyll a/b-bi
85	19.5	19.7	20	2	PC2084	serine proteinase
86	19.5	19.7	23	2	A44824	sodium channel III
87	19.5	19.7	25	2	B60840	somatostatin-25 -
88	19	19.2	6	2	IS1434	H4 histone - Afric
89	19	19.2	9	2	PT0324	Ig heavy chain CRD
90	19	19.2	10	2	PT0213	T-cell receptor al
91	19	19.2	10	2	P00785	NADH2 dehydrogenas
92	19	19.2	11	2	S65395	chemical-sense-rel
93	19	19.2	12	2	S36902	Em protein - wheat
94	19	19.2	12	2	S16204	6-phosphofructokin
95	19	19.2	12	2	C30503	Ig gamma-2b chain
96	19	19.2	12	2	PH0931	T-cell receptor be
97	19	19.2	13	2	A23695	myosin heavy chain
98	19	19.2	13	2	S52356	hypothetical prote
99	19	19.2	13	2	S54344	glyceraldehyde-3-p
100	19	19.2	14	2	S65392	cytochrome-c oxida
101	19	19.2	15	2	C37765	hypothetical prote
102	19	19.2	15	2	S36889	ribosomal protein

103	19	19.2	15	2	PA0091	methionine adenosy	176	18	18.2	20	2	A40451	dormancy-related p
104	19	19.2	15	2	PH1342	Ig heavy chain DJ	177	18	18.2	20	2	P00684	photosystem I 15.9
105	19	19.2	15	2	A27504	histone H2A - mouse	178	18	18.2	20	2	S19615	globin - polychaet
106	19	19.2	17	2	A61321	histone H4 - commo	179	18	18.2	21	2	S32883	DNA gyrase chain A
107	19	19.2	17	2	B61321	histone H4 - chick	180	18	18.2	22	2	A61497	seed protein ws-12
108	19	19.2	17	2	B44923	carboxypeptidase 3	181	18	18.2	22	2	F23734	insulin-like growt
109	19	19.2	17	2	A61211	anantin - Streptom	182	18	18.2	22	2	B35372	unidentified low M
110	19	19.2	18	2	S23950	45K protein - pig	183	18	18.2	22	2	A37043	Ig light chain, po
111	19	19.2	17	2	PRO332	Ig heavy chain CRD	184	18	18.2	22	2	A39324	hypothetical prote
112	19	19.2	20	2	S68620	histone H4 - sea u	185	18	18.2	23	2	A39855	paralytic peptide
113	19	19.2	20	2	S06149	photosystem I chai	186	18	18.2	23	2	S13268	heat shock protein
114	19	19.2	20	2	A60365	trypsin inhibitor	187	18	18.2	23	2	E43253	nuclear antigen EB
115	19	19.2	20	2	S68617	histone H2A - sea	188	18	18.2	23	2	PX0070	nuclear antigen P3
116	19	19.2	20	2	A55899	basement membrane	189	18	18.2	23	2	A48845	sterol regulatory
117	19	19.2	20	2	S78419	ribosomal protein	190	18	18.2	24	2	F24406	unspecific monooxy
118	19	19.2	21	2	PN0082	sperm chromatin pr	191	18	18.2	24	2	S10601	dimethylalanine mo
119	19	19.2	21	2	A02903	alpha-crystallin c	192	18	18.2	24	2	PN0172	serine proteinase
120	19	19.2	22	2	S52357	hypothetical prote	193	18	18.2	24	2	S07645	hst-omega protein
121	19	19.2	23	2	S38738	lipid transfer pro	194	18	18.2	25	2	E37520	glutathione transf
122	19	19.2	23	2	S15431	histone H4-1 precu	195	18	18.2	25	2	PQ0683	photosystem I 16.1
123	19	19.2	23	2	S54773	neural cell adhesi	196	18	18.2	25	2	D49253	nuclear antigen EB
124	19	19.2	23	2	S72535	probable acr-2 reg	197	18	18.2	25	2	PRO287	Ig heavy chain CRD
125	19	19.2	24	2	A56631	paralytic peptide	198	17.5	17.7	20	2	D49164	chromogranin-B - r
126	19	19.2	24	2	B43295	histone H4 - alfal	199	17.5	17.7	22	2	S04228	N4-(beta-N-acetyl)
127	19	19.2	24	2	S53749	histone H4 - rat	200	17	17.2	5	2	PT0608	T-cell receptor be
128	19	19.2	24	2	JP0052	ribosomal protein	201	17	17.2	7	2	E61491	angiotensin-conver
129	19	19.2	24	2	S70329	omega 1-40 secalin	202	17	17.2	8	2	A31570	seed protein ws-5
130	19	19.2	24	2	B39433	ada 3'-region alKB	203	17	17.2	8	2	PT0279	Ig heavy chain CRD
131	19	19.2	24	2	I38253	T-cell acute lymph	204	17	17.2	9	2	E41976	callisFRamide 5 -
132	19	19.2	25	2	S15155	protein-tyrosine k	205	17	17.2	10	1	GMROL2	leucosulfafakinin-II
133	19	19.2	25	2	A45920	cellulase (EC 3.2.	206	17	17.2	10	2	I60588	sperm-activating p
134	19	19.2	25	2	PS0145	histone H2B - sea	207	17	17.2	10	2	B60656	leucosulfafakinin II
135	19	19.2	25	2	JP0045	ribosomal protein	208	17	17.2	10	2	A42089	transcription fact
136	19	19.2	25	2	T09385	rev protein - huma	209	17	17.2	10	2	B56899	serum heterodimer,
137	19	19.2	25	2	S63484	coenzyme F420 hyd	210	17	17.2	10	2	B24736	inhibin beta-B cha
138	19	19.2	25	2	S47190	T-cell receptor J-	211	17	17.2	11	1	GMROL	leucosulfafakinin -
139	19	19.2	25	2	S39360	CDK inhibitor - mo	212	17	17.2	11	2	PT0081	protein QA300023 -
140	18.5	18.7	23	2	A41263	kinase-related tra	213	17	17.2	11	2	A60656	persulfafakinin - A
141	18	18.2	7	2	PT0246	Ig heavy chain CRD	214	17	17.2	12	2	PH1587	Ig H chain V-D-J r
142	18	18.2	9	2	D28854	fibriopeptide B -	215	17	17.2	13	1	MTCMAD	melanotropin alpha
143	18	18.2	9	2	S78420	ribosomal protein	216	17	17.2	13	1	MTCHOAD	melanotropin alpha
144	18	18.2	9	2	S39437	D-amin-acid oxida	217	17	17.2	13	2	S57571	T-cell receptor al
145	18	18.2	11	2	A26120	6-phosphofructokin	218	17	17.2	13	2	S47356	T-cell antigen rec
146	18	18.2	11	2	S45698	gamma-MSH-like pro	219	17	17.2	14	2	I51430	hemoglobin beta ch
147	18	18.2	11	2	C38887	T-cell receptor ga	220	17	17.2	14	2	I51432	histone H4-I precu
148	18	18.2	12	2	S34447	binr protein - Sta	221	17	17.2	14	2	A56632	neosulfafakinin-II -
149	18	18.2	12	2	S68402	NAD(+)-glycohydrol	222	17	17.2	14	2	S36678	dodecenoyl-CoA Del
150	18	18.2	13	2	S33800	chaperone, TCP1-re	223	17	17.2	14	2	S29878	Na+/K+-exchanging
151	18	18.2	13	2	S23372	T-cell receptor al	224	17	17.2	15	2	S13973	chlorophyll a/b-bi
152	18	18.2	14	2	PH1311	Ig heavy chain DJ	225	17	17.2	15	2	PC2215	fibriogenolytic p
153	18	18.2	14	2	PH1321	Ig heavy chain DJ	226	17	17.2	15	2	A49480	major immunophilin
154	18	18.2	14	4	I52618	hemoglobin beta ch	227	17	17.2	15	2	PH1310	Ig heavy chain DJ
155	18	18.2	15	2	PA0055	protein QP200007 -	228	17	17.2	15	2	S51735	T-cell receptor be
156	18	18.2	15	2	A61247	calcium-binding pr	229	17	17.2	15	2	A56963	acid phosphatase (
157	18	18.2	15	2	A56049	urogenital tumor m	230	17	17.2	16	2	S01669	rRNA N-glycosidase
158	18	18.2	15	2	PT0091	H+-transporting tw	231	17	17.2	16	2	S28433	major outer membra
159	18	18.2	16	2	PT0296	Ig heavy chain CDR	232	17	17.2	16	2	F49039	T-cell receptor be
160	18	18.2	16	2	H49039	T-cell receptor be	233	17	17.2	16	2	JN0264	translation initia
161	18	18.2	18	2	B34473	calcium-binding pr	234	17	17.2	16	2	PH1580	Ig H chain V-D-J r
162	18	18.2	18	2	A32917	protein phosphatas	235	17	17.2	17	2	S20490	photosystem II chl
163	18	18.2	19	2	C40634	orf21 5' of eryk	236	17	17.2	17	2	PH1357	Ig heavy chain DJ
164	18	18.2	19	2	PC1324	hypothetical prote	237	17	17.2	17	2	PD0005	very-high-density
165	18	18.2	19	2	PC1322	hypothetical prote	238	17	17.2	17	2	AF2093	heterocyst-inhibit
166	18	18.2	19	2	A49254	TcR delta chain V-	239	17	17.2	18	1	MTROB	melanotropin beta
167	18	18.2	19	2	S65435	mannanase peroxida	240	17	17.2	18	2	A36133	hypothetical prote
168	18	18.2	19	2	S65434	mannanase peroxida	241	17	17.2	18	2	S70612	alpha-macroglobuli
169	18	18.2	20	2	S32502	calpain (EC 3.4.22	242	17	17.2	18	2	S54272	CRC 75 protein - h
170	18	18.2	20	2	G61491	seed protein ws-25	243	17	17.2	18	2	S47196	T-cell receptor J-
171	18	18.2	20	2	JP0055	ribosomal protein	244	17	17.2	18	2	I49408	cytochrome-c oxida
172	18	18.2	20	2	DIRT	dental fluid tra	245	17	17.2	19	2	S20289	glutathione transf
173	18	18.2	20	2	S33001	hypothetical prote	246	17	17.2	19	2	S32548	pepsin-like protei
174	18	18.2	20	2	PC4385	GroEL protein homo	247	17	17.2	19	2	A92058	
175	18	18.2	20	2	PC4386	GroEL protein homo	248	17	17.2	19	2	S02269	glycogen(starch) s

249	17	17.2	19	2	S63485	coenzyme F420 hydr	322	16	16.2	10	2	A27617	tiiose-phosphate i
250	17	17.2	19	2	S29212	protein C - oat (f	323	16	16.2	10	2	H37196	bradykinin-potentl
251	17	17.2	20	2	A39328	notechis II-5b non	324	16	16.2	11	2	A14454	6-phosphofructokin
252	17	17.2	20	2	B61333	chymotrypsin (EC 3	325	16	16.2	12	2	S26548	T-cell receptor be
253	17	17.2	20	2	A49164	chromogranin-B - r	326	16	16.2	12	2	S65629	protoporphyrinogen
254	17	17.2	20	2	S68619	histone H3 - sea u	327	16	16.2	12	2	S10626	lipovitelin - Afr
255	17	17.2	20	2	E39419	collagen alpha 5(I	328	16	16.2	12	2	PR0228	Ig heavy chain CDR
256	17	17.2	20	2	S00315	photosystem I chai	329	16	16.2	12	2	PH1461	T-cell receptor be
257	17	17.2	20	2	S63483	coenzyme F420 hydr	330	16	16.2	13	1	XAV19B	angiotensin-conver
258	17	17.2	20	2	S57286	translational elonga	331	16	16.2	13	2	A32734	enkephalin precurs
259	17	17.2	20	2	S06150	photosystem I chai	332	16	16.2	13	2	S78519	ribosomal protein
260	17	17.2	20	2	S19616	globin - polychaet	333	16	16.2	13	2	D39690	neural cell adhesi
261	17	17.2	20	2	S53440	glutathione-bindin	334	16	16.2	13	2	B58533	CD61 homoloig - cha
262	17	17.2	20	2	S43627	cytochrome-c oxida	335	16	16.2	13	2	PR0331	Ig heavy chain CRD
263	17	17.2	20	2	I55663	MHC HLA-DR gamma	336	16	16.2	13	2	PH0796	T-cell receptor al
264	17	17.2	20	2	A41437	alpha-1-antiprotei	337	16	16.2	13	2	PH0799	T-cell receptor al
265	17	17.2	20	2	PC4387	GroEL protein homo	338	16	16.2	13	2	PH0783	T-cell receptor al
266	17	17.2	21	2	S33287	DNA polymerase - T	339	16	16.2	14	2	S27140	hypothetical prote
267	17	17.2	21	2	S47189	T-cell receptor J-	340	16	16.2	14	2	PA0096	pyruvate decarboxy
268	17	17.2	21	2	J02196	hypothetical 2.5k	341	16	16.2	14	2	E61308	hemocyanin chain 3
269	17	17.2	21	2	A60684	L-ascorbate peroxi	342	16	16.2	14	2	S43629	cytochrome-c oxida
270	17	17.2	21	2	S31427	biliary glycoprote	343	16	16.2	14	2	I64815	carbonic anhydrase
271	17	17.2	21	2	A20359	translational elonga	344	16	16.2	14	2	PH1332	Ig heavy chain DJ
272	17	17.2	22	2	PH1359	Ig heavy chain DJ	345	16	16.2	14	2	PH1322	Ig heavy chain DJ
273	17	17.2	22	2	S47195	T-cell receptor J-	346	16	16.2	14	2	E49039	T-cell receptor be
274	17	17.2	22	2	A45913	plantaricin A - La	347	16	16.2	15	2	PR0681	photosystem I 19.0
275	17	17.2	22	2	S21275	trypsin (EC 3.4.2	348	16	16.2	15	2	C56979	collagen alpha 1(I
276	17	17.2	23	2	B45220	glia-activating fa	349	16	16.2	15	2	S36896	ribosomal protein
277	17	17.2	23	2	C56978	collagen alpha 1(I	350	16	16.2	15	2	PA0018	photosystem I 9k p
278	17	17.2	23	2	I55406	nicotinic acetylch	351	16	16.2	15	2	S67975	apolipoprotein CB2
279	17	17.2	23	2	S16361	opacity protein P.	352	16	16.2	15	2	G41299	T-cell receptor al
280	17	17.2	23	2	A56272	conjugation induc	353	16	16.2	15	2	B49655	T-cell-receptor be
281	17	17.2	23	2	S33889	hypothetical prote	354	16	16.2	15	2	B56978	collagen alpha 2(X
282	17	17.2	23	4	JF0016	probable 2.9k prot	355	16	16.2	15	2	A53594	calnexin - mouse
283	17	17.2	24	1	BMTD	bombinin - Bombina	356	16	16.2	15	2	PH0775	T-cell receptor al
284	17	17.2	24	2	S11384	thrombin - Bombina	357	16	16.2	15	2	PH0779	T-cell receptor al
285	17	17.2	24	2	I46513	thrombin I - rabbi	358	16	16.2	15	2	C44101	calmodulin, vasoac
286	17	17.2	24	2	D53402	gltx 5'-region con	359	16	16.2	15	4	I38336	leucine-enkephalin
287	17	17.2	24	2	PR0076	hypothetical prote	360	16	16.2	16	1	MRP8S	melanotropin beta
288	17	17.2	24	2	T07991	S locus-linked pro	361	16	16.2	16	2	C45133	casein kinase II
289	17	17.2	24	2	T08160	endosperm protein,	362	16	16.2	16	2	A27803	myosin light chain
290	17	17.2	24	2	S70333	glucan 1,3-beta-gl	363	16	16.2	16	2	H29501	fibronopeptide A -
291	17	17.2	24	2	S56003	chymotrypsin (EC 3	364	16	16.2	16	2	C44896	heat shock protein
292	17	17.2	25	2	A45109	trypsin (EC 3.4.2	365	16	16.2	16	2	S01104	hypothetical prote
293	17	17.2	25	2	A23698	lysozyme (EC 3.4.2	366	16	16.2	16	2	J70609	leukocyte chemoatc
294	17	17.2	25	2	S10850	alpha-amylase inhi	367	16	16.2	16	2	PH0773	T-cell receptor be
295	17	17.2	25	2	A18864	enkephalin-contain	368	16	16.2	17	1	A61339	vesiculakxin I - e
296	17	17.2	25	2	DA1575	bombinin-like pept	369	16	16.2	17	2	S17274	ribosomal protein
297	17	17.2	25	2	JH0700	omega-conotoxin MV	370	16	16.2	17	2	PC1318	large granule L6 c
298	17	17.2	25	2	S47204	T-cell receptor J-	371	16	16.2	17	2	I24687	T-cell receptor be
299	17	17.2	25	2	S65729	hemoglobin, extrac	372	16	16.2	17	2	A37823	dihydrolipoamide S
300	17	17.2	25	2	E41839	ribosomal protein	373	16	16.2	17	2	S10786	enamelin, 26k - bo
301	17	17.2	25	2	S77862	hypothetical prote	374	16	16.2	17	2	C84063	translational elonga
302	17	17.2	25	2	B69274	glutathione transf	375	16	16.2	18	2	S39153	ribosomal protein
303	17	17.2	25	2	A23605	histone H1.1 - whe	376	16	16.2	18	2	S49026	protein Pf6 - gold
304	17	17.2	25	2	A61499	glutathione transf	377	16	16.2	18	2	D59137	INS150A/INS150B mu
305	17	17.2	25	2	S03456	T-cell receptor al	378	16	16.2	18	4	S40664	Ig kappa chain V r
306	17	17.2	25	2	PC4445	L-ascorbate peroxi	379	16	16.2	19	2	A28814	ubiquitin - Thermo
307	17	17.2	25	2	S56002	glucan 1,3-beta-gl	380	16	16.2	19	2	S34459	cytochrome c(EDH)
308	16.5	16.7	21	2	B29663	histone H2B - star	381	16	16.2	19	2	J29057	ribosomal protein
309	16.5	16.7	23	2	S47194	T-cell receptor J-	382	16	16.2	19	2	S59717	hypothetical prote
310	16.5	16.7	24	2	B42266	peptidylglycine mo	383	16	16.2	19	2	S19613	globin - polychaet
311	16.5	16.7	24	2	S34405	adenylate kinase	384	16	16.2	19	2	A13361	cAMP-regulated pho
312	16	16.2	5	2	PR0553	T-cell receptor be	385	16	16.2	19	2	S78411	ribosomal protein
313	16	16.2	8	2	T48890	hypothetical prote	386	16	16.2	19	2	B53875	5-carboxymethyl-2-
314	16	16.2	8	2	PR0554	T-cell receptor be	387	16	16.2	20	2	B53875	creatinase kinase
315	16	16.2	9	2	B45020	probable minipoly	388	16	16.2	20	2	S00492	hemocyanin chain I
316	16	16.2	9	2	B41983	orf downstream to b	389	16	16.2	20	2	GC1570	gamma-crystallin
317	16	16.2	9	2	I50633	c-rel protein - ch	390	16	16.2	20	2	JN0252	water-soluble 35k
318	16	16.2	9	2	S26508	collagen alpha 2(V	391	16	16.2	20	2	S65399	immunodeficiency v
319	16	16.2	9	2	PC7078	unidentified 48.7k	392	16	16.2	20	2	I65242	hemocic protein H
320	16	16.2	10	2	S65388	cytochrome-c oxida	393	16	16.2	20	2	T50757	pufk protein [limpo
321	16	16.2	10	2	S24190	tryptase (EC 3.4.2	394	16	16.2	20	2		

395	16	16.2	20	2	S71017	hypoethetical prote
396	16	16.2	20	2	P00046	citrate (sl)-synh
397	16	16.2	20	2	S32387	ribosomal protein
398	16	16.2	20	2	T26748	hypoethetical prote
399	16	16.2	20	2	A48406	annexin VI homolog
400	16	16.2	20	2	A60812	plasma proteiase
401	16	16.2	20	2	E54226	light-harvesting p
402	16	16.2	21	2	S25603	NADH2 dehydrogens
403	16	16.2	21	2	A32521	hexokinase (EC 2.7
404	16	16.2	21	2	A38837	T-cell receptor be
405	16	16.2	21	2	PH1690	Ig heavy chain V r
406	16	16.2	21	2	E44101	calmodulin, vasoac
407	16	16.2	21	2	S28436	major outer membra
408	16	16.2	21	2	S39455	34K ribonucleoprot
409	16	16.2	21	2	C31182	hypoethetical 2.4K
410	16	16.2	21	2	S22875	tya protein - years
411	16	16.2	21	2	S62893	cold-Inducible pro
412	16	16.2	21	2	I54268	alpha-1-antichymot
413	16	16.2	21	2	B49200	cystatin-related p
414	16	16.2	21	2	I53263	CRP-1 delta - rat
415	16	16.2	21	2	T12935	hypoethetical prote
416	16	16.2	22	2	A26376	peptidyl-dipectia
417	16	16.2	22	2	B48395	probable angiotens
418	16	16.2	22	2	C38839	histone H2B - sea
419	16	16.2	22	2	B40288	chaperonin 10 - Rh
420	16	16.2	22	2	PQ0667	photosystem I 19.3
421	16	16.2	22	2	S67974	apolipoprotein Cpl
422	16	16.2	22	2	A22441	tumor necrosis fac
423	16	16.2	22	2	B48732	NADH2 dehydrogenas
424	16	16.2	23	2	JP0062	ribosomal protein
425	16	16.2	23	2	B04348	internal peptide V
426	16	16.2	23	2	G64520	hypoethetical prote
427	16	16.2	23	2	T44539	hypoethetical prote
428	16	16.2	23	2	S37491	hypoethetical prote
429	16	16.2	23	2	A60226	pyruvate dehydroge
430	16	16.2	24	2	S23631	cytochrome-c oxida
431	16	16.2	24	2	A33262	heparin-binding gr
432	16	16.2	24	2	I45851	adenosylmethionine
433	16	16.2	24	2	PH1909	T-cell receptor al
434	16	16.2	24	2	S51064	ribosomal protein
435	16	16.2	24	2	B56978	collagen alpha 2(X
436	16	16.2	24	2	A05298	fibrinogen gamma c
437	16	16.2	24	2	S10681	probable 7-ethoxyc
438	16	16.2	24	2	S35641	DNA (cytosine-5')-
439	16	16.2	24	2	F45357	Kex2/subtilisin-11
440	16	16.2	24	2	C45357	Kex2/subtilisin-11
441	16	16.2	24	2	A64023	hypoethetical prote
442	16	16.2	25	2	S22221	peroxidase (EC 1.1
443	16	16.2	25	2	JH0701	omega-conotoxin MV
444	16	16.2	25	2	F49533	T-cell receptor be
445	16	16.2	25	2	S58385	T-cell receptor al
446	16	16.2	25	2	S26233	ribosomal protein
447	16	16.2	25	2	T06233	ribosomal protein
448	16	16.2	25	2	I38002	calcium channel be
449	16	16.2	25	2	S00329	beta-N-acetylgluco
450	16	16.2	25	2	A60286	heat-stable serine
451	16	16.2	25	2	T09588	MADS box protein P
452	16	16.2	25	2	C25629	cytochrome-c oxida
453	16	16.2	25	2	S71387	alpha-2-macroglobu
454	16	16.2	25	2	S22234	vitronectin - chic
455	16	16.2	25	2	B86074	hypoethetical prote
456	16	16.2	25	2	A56864	membrane alaanyl a
457	15.5	15.7	14	2	PA0045	porin porI - Arabi
458	15.5	15.7	18	2	A35704	cytochrome P450 ol
459	15.5	15.7	12	2	S78007	fucoyltransferase
460	15.5	15.7	22	2	S55236	T669 kinase - huma
461	15.5	15.7	23	2	I50174	collagen alpha 1(I
462	15.5	15.7	24	2	PH1696	Ig heavy chain V r
463	15	15.2	3	4	GKHU	growth-modulating
464	15	15.2	7	2	A35039	hypoethetical colla
465	15	15.2	7	2	A44428	platelet aggregati
466	15	15.2	7	2	PT0579	T-cell receptor mo
467	15	15.2	7	2	A38671	peptidylglycine de
468	15	15.2	8	2	A21440	variant surface g1
469	15	15.2	8	2	I48934	apolipoprotein A-I
470	15	15.2	8	2	PT0691	T-cell receptor be
471	15	15.2	9	2	PT0288	Ig heavy chain CRD
472	15	15.2	9	2	A37027	macrophage chemota
473	15	15.2	9	2	C60070	gastrin - domestic
474	15	15.2	10	2	S09387	PVI protein - huma
475	15	15.2	10	2	S70721	heat shock protein
476	15	15.2	10	2	S43631	cytochrome-c oxida
477	15	15.2	10	2	S77990	cytochrome-c oxida
478	15	15.2	10	2	PT0289	Ig heavy chain CRD
479	15	15.2	10	2	PH0894	T-cell receptor be
480	15	15.2	11	2	D61033	ranatathyrkinin D -
481	15	15.2	11	2	S45386	low density lipopr
482	15	15.2	11	1	JTG50	temrogen A-10 -
483	15	15.2	12	2	C36201	1-aminocyclopropan
484	15	15.2	12	2	PH1675	Ig heavy chain V r
485	15	15.2	12	2	A39233	myosin heavy chain
486	15	15.2	12	2	A44874	proboosipedia - fir
487	15	15.2	12	2	G49215	urease (EC 3.5.1.5
488	15	15.2	12	2	S49547	hypoethetical prote
489	15	15.2	12	2	A35585	cytokinin-binding
490	15	15.2	12	2	A55837	5-aminimidazole r
491	15	15.2	12	2	S43170	kinesin light chal
492	15	15.2	12	2	PH1180	T-cell receptor al
493	15	15.2	12	2	PH0802	T-cell receptor al
494	15	15.2	12	2	PH0790	T-cell receptor al
495	15	15.2	12	4	PC2123	amino transferase c
496	15	15.2	13	2	PH1676	Ig heavy chain V r
497	15	15.2	13	2	S46210	collagen alpha 1(V
498	15	15.2	13	2	PC1008	40K extracellular
499	15	15.2	13	2	S28425	20K protein - rape
500	15	15.2	13	2	S47390	T-cell antigen rec
501	15	15.2	13	2	PH0788	T-cell receptor al
502	15	15.2	14	1	BSRD	bombesin - fire-be
503	15	15.2	14	1	LFECW	trp operon leader
504	15	15.2	14	1	LFEBWC	trp operon leader
505	15	15.2	14	1	LFEBWT	trp operon leader
506	15	15.2	14	2	PH1677	Ig heavy chain V r
507	15	15.2	14	2	E90858	trp operon leader
508	15	15.2	14	2	S74128	superoxide dismuta
509	15	15.2	14	2	PQ0152	18K iron-sulfur pr
510	15	15.2	14	2	PT0294	Ig heavy chain CRD
511	15	15.2	14	2	PH1348	Ig heavy chain DJ
512	15	15.2	14	2	PH1356	Ig heavy chain DJ r
513	15	15.2	14	2	PH1597	Ig H chain V-D-J r
514	15	15.2	14	2	PH0792	T-cell receptor al
515	15	15.2	14	2	A23996	beta-granulin - rat
516	15	15.2	14	2	PH0915	T-cell receptor be
517	15	15.2	14	2	B85761	trp operon leader
518	15	15.2	15	2	S26524	T-cell receptor al
519	15	15.2	15	2	S36888	ribosomal protein
520	15	15.2	15	2	PQ0017	terminal protein -
521	15	15.2	15	2	A60929	dichloromethane de
522	15	15.2	15	2	B60929	dichloromethane de
523	15	15.2	15	2	S71920	protease ECP 32
524	15	15.2	15	2	PA0051	protein QP20016 -
525	15	15.2	15	2	A32971	heparin-binding le
526	15	15.2	15	2	PH1365	Ig heavy chain DJ
527	15	15.2	15	2	S05700	insulin-like growt
528	15	15.2	15	2	S57577	T cell receptor V-
529	15	15.2	15	2	PN0665	T cell receptor V-
530	15	15.2	15	2	F44833	synaptosomal-assoc
531	15	15.2	15	2	PD0444	coupling factor 6
532	15	15.2	15	2	I76838	fl3 ligand isofor
533	15	15.2	15	2	PH0751	T-cell receptor be
534	15	15.2	15	2	G35141	T-cell receptor de
535	15	15.2	15	2	PA0041	plastoquinol-plast
536	15	15.2	15	4	I38032	hypoethetical MN1/T
537	15	15.2	15	4	I38031	hypoethetical MN1/T
538	15	15.2	16	2	G29501	fibrinopeptide A -
539	15	15.2	16	2	S05703	homeotic protein c
540	15	15.2	16	2	D58501	26K kidney and gal

541	15	16	2	S09700	phycobilliprotein 1	614	15	15.2	20	2	B53592	Ht-exporting ATPas
542	15.2	16	2	B60278	24k antigen - Myco	615	15	15.2	21	2	A41154	ethylene-forming e
543	15.2	16	2	B44896	heat shock protein	616	15	15.2	21	2	S68023	nucleoside-diphosp
544	15.2	16	2	G24304	ribosomal protein	617	15	15.2	21	2	A27719	trypsin (EC 3.4.21
545	15.2	16	2	A41170	photosystem II 6.1	618	15	15.2	21	2	A61413	interferon alpha (
546	15.2	16	2	PA0103	L-lactate dehydrog	619	15	15.2	21	2	PH1688	Ig heavy chain V r
547	15.2	16	2	C49048	T-cell receptor be	620	15	15.2	21	2	S02643	RNA-directed RNA p
548	15.2	16	2	A49255	T-cell receptor be	621	15	15.2	21	2	JH0361	carrasin - goldfis
549	15.2	16	2	PH1638	Ig H chain V-D-J r	622	15	15.2	21	2	JU0386	nitrile hydratase
550	15.2	16	2	D49037	Tcr delta chain V-	623	15	15.2	21	2	A59325	probable bacteriop
551	15.2	16	2	A61530	triiose-phosphate i	624	15	15.2	21	2	S78416	ribosomal protein
552	15.2	16	2	D83865	hypothetical prote	625	15	15.2	21	2	A59429	dart gland peptide
553	15.2	16	4	A33171	hypothetical prote	626	15	15.2	22	2	C46285	formaldehyde dehyd
554	15.2	17	2	C37520	glutathione transf	627	15	15.2	22	2	S58433	isocitrate dehydro
555	15.2	17	2	B20242	pyruvate kinase (E	628	15	15.2	22	2	PH1325	interferon alpha (
556	15.2	17	2	B61334	trypsin (EC 3.4.21	629	15	15.2	22	2	PH1678	Ig heavy chain V r
557	15.2	17	2	S26744	Ig heavy chain J r	630	15	15.2	22	2	PH1679	Ig heavy chain V r
558	15.2	17	2	PH1754	T-cell receptor al	631	15	15.2	22	2	PH1721	Ig heavy chain V r
559	15.2	17	2	JP0046	ribosomal protein	632	15	15.2	22	2	PH1721	ribosomal protein
560	15.2	17	2	A34835	ribosomal protein	633	15	15.2	22	2	JP0071	collagen alpha 1(I
561	15.2	17	2	I58087	ryanodine receptor	634	15	15.2	22	2	D56978	GTP-binding, regula
562	15.2	17	2	A61518	unidentified prote	635	15	15.2	22	2	I45904	hypothetical prote
563	15.2	17	2	D22595	bombolitin IV - Am	636	15	15.2	22	2	S73389	T-cell receptor be
564	15.2	17	2	A60570	Ig mu heavy chain	637	15	15.2	22	2	PH1912	T-cell receptor J-
565	15.2	17	2	S57556	T-cell receptor be	638	15	15.2	22	2	S47209	albumin - rat (fra
566	15.2	17	2	PH0757	ribosomal protein	639	15	15.2	22	2	I51830	folate binding pro
567	15.2	18	2	S78421	Ig heavy chain DJ	640	15	15.2	22	2	S62670	hypothetical prote
568	15.2	18	2	PH1368	Ig heavy chain DJ	641	15	15.2	22	2	H83991	NADH2 dehydrogenas
569	15.2	18	2	A24749	photosystem I prot	642	15	15.2	22	2	H49732	cytochrome-c oxida
570	15.2	18	2	S14661	neuropeptide A - b	643	15	15.2	23	2	S43632	paralytic peptide
571	15.2	18	2	I52623	Ig heavy chain DJ	644	15	15.2	23	2	B39855	cryptidin - mouse (
572	15.2	18	2	PH1349	T-cell receptor be	645	15	15.2	23	2	I48936	cryptidin - western
573	15.2	18	2	PH0768	T-cell receptor be	646	15	15.2	23	2	I49413	T-cell receptor J-
574	15.2	18	2	B48839	Tcr delta chain V-	647	15	15.2	23	2	S47192	Ig heavy chain DJ
575	15.2	18	2	G49037	Ig heavy chain DJ	648	15	15.2	23	2	PH1361	Ig heavy chain DJ
576	15.2	19	2	PH1304	Ig heavy chain DJ	649	15	15.2	23	2	PH1364	Ig heavy chain V r
577	15.2	19	2	PH1307	gamma crystallin I	650	15	15.2	23	2	PH1681	Ig heavy chain V r
578	15.2	19	2	A60894	beta-galactoside-b	651	15	15.2	23	2	PH1682	Ig heavy chain V r
579	15.2	19	2	PX0062	nitrogen fixation	652	15	15.2	23	2	PH1689	Ig heavy chain V r
580	15.2	19	2	S32675	ribosomal protein	653	15	15.2	23	2	PH1691	Ig heavy chain V r
581	15.2	19	2	JP0054	S-locus specific g	654	15	15.2	23	2	PH1693	Ig heavy chain V r
582	15.2	19	2	E56661	small granule S2 c	655	15	15.2	23	2	PH1694	Ig heavy chain V r
583	15.2	19	2	PC1309	transhyretin - bu	656	15	15.2	23	2	PH1695	Ig heavy chain V r
584	15.2	19	2	A49192	Ig heavy chain DJ	657	15	15.2	23	2	I33084	ribosomal protein
585	15.2	19	2	PH1360	phospholipase A2 (658	15	15.2	23	2	A61574	hyaluronic acid-bi
586	15.2	19	2	PS0332	hypothetical prote	659	15	15.2	23	2	B26091	leukocyte glycopro
587	15.2	19	2	S25715	Qa-2 antigen - mou	660	15	15.2	23	2	I51922	cystic fibrosis tr
588	15.2	19	2	S12268	Tcr delta chain V-	661	15	15.2	23	2	A04348	4-hydroxyphenylpyr
589	15.2	19	2	I49037	enhancing factor -	662	15	15.2	23	2	S74178	hypothetical prote
590	15.2	20	2	S29495	urease (EC 3.5.1.5	663	15	15.2	23	2	S32727	Ig heavy chain DJ
591	15.2	20	2	H49215	15K protein B - ra	664	15	15.2	23	2	PH1303	tyrosine kinase su
592	15.2	20	2	B38382	Ig heavy chain CDR	665	15	15.2	23	2	A56357	brain-type creatin
593	15.2	20	2	PM0248	ribosomal protein	666	15	15.2	24	2	B42272	alicyclic amine N-
594	15.2	20	2	JP0070	ribosomal protein	667	15	15.2	24	2	PC2199	phosphoprotein pho
595	15.2	20	2	JP0060	ribosomal protein	668	15	15.2	24	2	I53473	fatty acid-binding
596	15.2	20	2	JP0061	gamma crystallin V	669	15	15.2	24	2	PH0084	MSEL-neurophysin -
597	15.2	20	2	S07232	ribulose-bisphosph	670	15	15.2	24	2	B60422	relaxin - baboon (
598	15.2	20	2	D60894	lens fiber cell me	671	15	15.2	24	2	PT0258	Ig heavy chain CDR
599	15.2	20	2	E34490	lens fiber cell me	672	15	15.2	24	2	PT0258	Ig heavy chain CDR
600	15.2	20	2	C34490	Dnak protein homol	673	15	15.2	24	2	PT0258	Ig heavy chain V r
601	15.2	20	2	PC4384	jacalin beta-I cha	674	15	15.2	24	2	PH1683	Ig heavy chain V r
602	15.2	20	2	S29636	glutaryl-tRNA redu	675	15	15.2	24	2	PH1684	Ig heavy chain V r
603	15.2	20	2	S48702	glutathione S-trans	676	15	15.2	24	2	PH1685	Ig heavy chain V r
604	15.2	20	2	PC1152	glutathione S-trans	677	15	15.2	24	2	PH1698	Ig heavy chain V r
605	15.2	20	2	S19618	globin - polychaet	678	15	15.2	24	2	PH1711	Ig heavy chain V r
606	15.2	20	2	S28405	lamin B receptor -	679	15	15.2	24	2	PH1712	Ig heavy chain V r
607	15.2	20	2	S28405	Ig heavy chain DJ	680	15	15.2	24	2	PH1732	Ig heavy chain V r
608	15.2	20	2	PH1341	Ig heavy chain DJ	681	15	15.2	24	2	PH1697	Ig heavy chain V r
609	15.2	20	2	PH1338	neurofilament heav	682	15	15.2	24	2	PH1916	T-cell receptor be
610	15.2	20	2	I53671	T cell receptor al	683	15	15.2	24	2	A61141	calreticulin, panc
611	15.2	20	2	PH1783	82k protein - bovi	684	15	15.2	24	2	A61505	pollen allergen Ph
612	15.2	20	2	S31220	ribosomal protein	685	15	15.2	24	2	S02073	photosystem II 10k
613	15.2	20	2	S78763	ribosomal protein	686	15	15.2	24	2		

687	15	15.2	24	2	PC2312	X-Pro aminopeptidase	760	14	14.1	10	2	PX0060	lysosome-associate
688	15	15.2	24	2	PC2313	X-Pro aminopeptidase	761	14	14.1	10	2	A59173	nuclease BHL (EC 3
689	15	15.2	24	2	S37383	rRNA N-glycosidase	762	14	14.1	10	2	PA0116	ferredoxin-NADP re
690	15	15.2	24	2	T24611	hypothetical prote	763	14	14.1	10	2	PS0220	ferredoxin-NADP re
691	15	15.2	24	2	I54329	gene NF1 protein -	764	14	14.1	11	2	YHRT	morphogenetic neur
692	15	15.2	24	2	DB5955	hypothetical prote	765	14	14.1	11	2	YHNU	morphogenetic neur
693	15	15.2	24	2	G85602	hypothetical prote	766	14	14.1	11	2	YHNU	morphogenetic neur
694	15	15.2	25	1	JC4278	ribosomal protein	767	14	14.1	11	2	YHAXE	morphogenetic neur
695	15	15.2	25	1	PH1686	Ig heavy chain V r	768	14	14.1	11	2	YHAXE	morphogenetic neur
696	15	15.2	25	2	PH1700	Ig heavy chain V r	769	14	14.1	11	2	B58501	24K kidney and bla
697	15	15.2	25	2	PH1701	Ig heavy chain V r	770	14	14.1	11	2	A44755	20alpha-hydroxyste
698	15	15.2	25	2	S07770	histone H2B.1, spe	771	14	14.1	11	2	E41476	probable antigen 5
699	15	15.2	25	2	S49025	ribosomal protein	772	14	14.1	11	2	S19775	wound-induced prot
700	15	15.2	25	2	JF0044	ribosomal protein	773	14	14.1	11	2	S05002	corazonin - Americ
701	15	15.2	25	2	JQ1617	ribosomal protein	774	14	14.1	11	2	PH1343	Ig heavy chain DJ
702	15	15.2	25	2	JC4685	ribosomal protein	775	14	14.1	11	2	PH0209	T-cell receptor al
703	15	15.2	25	2	S38425	ribosomal protein	776	14	14.1	11	2	PH0217	T-cell receptor be
704	15	15.2	25	2	T49214	ribosomal protein	777	14	14.1	11	2	PH0947	T-cell receptor be
705	15	15.2	25	2	I56978	collagen alpha 2(X	778	14	14.1	11	2	PH0924	gene RSTR4 protei
706	15	15.2	25	2	A60921	uroepithelial cell	779	14	14.1	11	2	T52304	hypothetical prote
707	15	15.2	25	2	I67422	gene GLOU4 protein	780	14	14.1	11	2	H84082	urease (EC 3.5.1.5
708	15	15.2	25	2	S25434	gene CP41 leader p	781	14	14.1	12	2	C49215	collagen alpha 2(V
709	15	15.2	25	2	S13996	hypothetical prote	782	14	14.1	12	2	B46662	hypothetical 1.2K
710	15	15.2	25	2	S21515	flap protein - Esc	783	14	14.1	12	2	C39109	24K kidney and bla
711	15	15.2	25	2	JF0064	ribosomal protein	784	14	14.1	12	2	A58501	hypothetical prote
712	15	15.2	25	2	T01689	large granule RL c	785	14	14.1	12	2	C64030	DNA-binding protei
713	15	15.2	25	2	PC1314	large granule RL c	786	14	14.1	12	2	C34135	coagulation factor
714	15	15.2	25	2	S44201	HHA-DBI exon2 pro	787	14	14.1	12	2	A49261	T-cell antigen rec
715	15	15.2	18	2	B32473	histidine-rich pro	788	14	14.1	12	2	A47360	T-cell receptor be
716	14.5	14.6	19	2	A60152	acidolysin (EC 3.4	789	14	14.1	12	2	S51737	T-cell receptor be
717	14.5	14.6	20	2	A57106	hull allergen gly	790	14	14.1	12	2	C49033	insulin-like growth
718	14.5	14.6	22	2	S03459	T-cell receptor al	791	14	14.1	12	2	A60528	insulin-like growth
719	14.5	14.6	22	2	S48196	carbon-monoxide de	792	14	14.1	12	2	E20907	Ig kappa-2 chain J
720	14	14.1	4	2	PL0140	carbon-monoxide de	793	14	14.1	12	2	PH1635	Ig H chain V-D-J r
721	14	14.1	4	2	I38888	CoI intron 16 prot	794	14	14.1	12	2	S21163	NAD ADP-ribosyltra
722	14	14.1	5	2	S53595	hypothetical prote	795	14	14.1	13	2	A60409	bombosin-like pept
723	14	14.1	6	2	A61419	sarcosine dehydrog	796	14	14.1	13	2	A46463	preabsorbing anti
724	14	14.1	6	2	S29637	Jacalin beta-II ch	797	14	14.1	13	2	A61288	spore proteinase g
725	14	14.1	6	2	B56979	collagen alpha 1(I	798	14	14.1	13	2	JN0310	insulin-binding pr
726	14	14.1	7	2	S42407	gramicidin S synth	799	14	14.1	13	2	A23694	myosin heavy chain
727	14	14.1	7	2	B33541	hypothetical prote	800	14	14.1	13	2	A54326	granular kallikre
728	14	14.1	7	2	E33932	Ig mu chain D-regi	801	14	14.1	13	2	PR0256	Ig heavy chain CRD
729	14	14.1	7	2	S66442	glutathione S-tran	802	14	14.1	13	2	PR0263	T-cell antigen rec
730	14	14.1	7	2	S45648	Na+-transporting A	803	14	14.1	13	2	S47357	zona pellucida-bi
731	14	14.1	7	4	S15597	orf 4 rat 5'-regi	804	14	14.1	13	2	S10562	T-cell receptor be
732	14	14.1	8	2	S20162	leghemoglobin III	805	14	14.1	13	2	PH1479	T-cell receptor be
733	14	14.1	8	2	I64832	Ca2+-transporting	806	14	14.1	13	2	PH0928	collecting duct wa
734	14	14.1	9	2	S59902	glutathione transf	807	14	14.1	13	2	I51905	glycophorin B/glyc
735	14	14.1	9	2	S07205	litorin 2-Glu - Au	808	14	14.1	14	2	I70076	fibrinogen A -
736	14	14.1	9	2	S07204	litorin I - Austro	809	14	14.1	14	2	A32654	carbon-monoxide de
737	14	14.1	9	2	S07241	litorin - Robde's	810	14	14.1	14	2	PL0142	extension protein
738	14	14.1	9	2	CA1170	photosystem II pro	811	14	14.1	14	2	S48685	omega-glucanase 1
739	14	14.1	9	2	PT0285	Ig heavy chain CRD	812	14	14.1	14	2	PN0147	homeotic protein E
740	14	14.1	9	2	S65913	pyrimidine synthe	813	14	14.1	14	2	PN0151	cell surface allos
741	14	14.1	9	2	PC7076	spectrin alpha cha	814	14	14.1	14	2	A60770	sperm motility inh
742	14	14.1	10	2	AG1289	streptopain (EC 3.	815	14	14.1	14	2	S66234	thrombospondin 2 -
743	14	14.1	10	2	PC0177	neuromedin C - lau	816	14	14.1	14	2	DA5474	Ig H chain V-D-J r
744	14	14.1	10	2	A60647	neuromedin C - bov	817	14	14.1	14	2	PH1639	T-cell receptor al
745	14	14.1	10	2	H60787	sperm-activating p	818	14	14.1	14	2	PH0801	T-cell receptor be
746	14	14.1	10	2	H60787	sperm-activating p	819	14	14.1	14	2	PH0795	T-cell receptor be
747	14	14.1	10	2	D60788	sperm-activating p	820	14	14.1	14	2	PH0765	T-cell receptor be
748	14	14.1	10	2	B60787	sperm-activating p	821	14	14.1	14	2	PH0945	dehydrin 4.5K poly
749	14	14.1	10	2	A60788	sperm-activating p	822	14	14.1	14	2	PC4382	H+-transporting tw
750	14	14.1	10	2	C60589	sperm-activating p	823	14	14.1	14	2	F33160	ubiquinol-cytochro
751	14	14.1	10	2	D60588	sperm-activating p	824	14	14.1	15	2	S42741	S-luciferase
752	14	14.1	10	2	XGMBE	erythrocyte membra	825	14	14.1	15	2	B56661	collagen alpha 1(X
753	14	14.1	10	2	A46030	gonadoliberin I -	826	14	14.1	15	2	H56978	hypothetical 1.5K
754	14	14.1	10	2	A21114	gonadoliberin I -	827	14	14.1	15	2	B39109	33K variable histo
755	14	14.1	10	2	A30823	bohrpoxstoxin - ja	828	14	14.1	15	2	C41383	ribosomal protein
756	14	14.1	10	2	I48778	small nuclear ribo	829	14	14.1	15	2	T09463	seed storage prote
757	14	14.1	10	2	PT0632	T-cell receptor be	830	14	14.1	15	2	PA0009	29K protein 4228 -
758	14	14.1	10	2	PT0664	T-cell receptor be	831	14	14.1	15	2	PS0212	
759	14	14.1	10	2	PT0215	T-cell receptor be	832	14	14.1	15	2		

833	14	14.1	15	2	PA0062	fumarate hydratase	906	14	14.1	19	2	B29501	fibrinopeptide A -
834	14	14.1	15	2	A36279	chemottractant pr	907	14	14.1	19	2	C29501	fibrinopeptide A -
835	14	14.1	15	2	A36527	juvenile-hormone e	908	14	14.1	19	2	B56613	vitronectin
836	14	14.1	15	2	S43634	cytochrome-c oxida	909	14	14.1	19	2	PA0010	seed storage prote
837	14	14.1	15	2	S57201	basic proteinase I	910	14	14.1	19	2	H61491	seed protein ws-24
838	14	14.1	15	2	PH1314	Ig heavy chain DJ	911	14	14.1	19	2	T50329	wd-repeat protein
839	14	14.1	15	2	S03955	acidic fibroblast	912	14	14.1	19	2	G60977	14-3-3 protein hom
840	14	14.1	15	2	PQ0073	T-cell receptor be	913	14	14.1	19	2	JX0124	tachyplesin I prec
841	14	14.1	15	2	PQ0074	T-cell receptor be	914	14	14.1	19	2	S60110	hypothetical prote
842	14	14.1	15	2	PT0097	glutathione peroxi	915	14	14.1	19	2	I49039	T-cell receptor be
843	14	14.1	15	2	PH1616	Ig H chain V-D-J r	916	14	14.1	19	2	A44356	37k adherens junct
844	14	14.1	15	2	PH0780	T-cell receptor al	917	14	14.1	19	2	S22232	vitronectin - goat
845	14	14.1	15	2	PH0806	T-cell receptor al	918	14	14.1	19	2	S22233	vitronectin - shee
846	14	14.1	15	2	PH0797	T-cell receptor al	919	14	14.1	19	2	S43045	translation elonga
847	14	14.1	15	2	E49037	TcR delta chain V-	920	14	14.1	20	2	A60728	cytochrome p450 3A
848	14	14.1	15	2	S71306	heat shock protein	921	14	14.1	20	2	S17461	flavodoxin B - Azo
849	14	14.1	15	2	S71396	dhindripyrimidine	922	14	14.1	20	2	A54083	p190/210, fatty ac
850	14	14.1	15	2	S66443	NAD(P) transhydrog	923	14	14.1	20	2	S29100	glutathione transf
851	14	14.1	15	2	PQ0780	NADH2 dehydrogenas	924	14	14.1	20	2	A14344	alanine transamina
852	14	14.1	16	2	S17217	ribulose-bisphosph	925	14	14.1	20	2	A60489	venombin A (EC 3.4
853	14	14.1	16	2	A28144	ribosomal protein	926	14	14.1	20	2	D49215	urease (EC 3.5.1.5
854	14	14.1	16	2	S02473	coat protein Vp1 -	927	14	14.1	20	2	S46488	peptidylprolyl iso
855	14	14.1	16	2	B58501	25k kidney and gal	928	14	14.1	20	2	PX0059	trypsin inhibitor
856	14	14.1	16	2	S51610	hypothetical prote	929	14	14.1	20	2	S50741	probable trypsin i
857	14	14.1	16	2	P50210	28k protein 4209 -	930	14	14.1	20	2	B60505	hemoglobin Al-2 be
858	14	14.1	16	2	S28213	glutathione transf	931	14	14.1	20	2	D37396	gamma-crystallin I
859	14	14.1	16	2	A35552	caldesmon - turke	932	14	14.1	20	2	A39543	pollen allergen Fe
860	14	14.1	16	2	PT0224	Ig heavy chain CDK	933	14	14.1	20	2	A44927	collagen alpha 1(I
861	14	14.1	16	2	PH1351	Ig heavy chain DJ	934	14	14.1	20	2	S60668	major outer membra
862	14	14.1	16	2	PH1317	Ig heavy chain DJ	935	14	14.1	20	2	S65746	hypothetical prote
863	14	14.1	16	2	B48406	annexin VI homolog	936	14	14.1	20	2	T48881	hypothetical prote
864	14	14.1	16	2	PH1453	T-cell receptor al	937	14	14.1	20	2	B39089	leader peptide fjm
865	14	14.1	16	2	S10678	aldenhyde dehydrog	938	14	14.1	20	2	S18582	hydrogenase (EC 1.
866	14	14.1	16	2	D89854	conserved hypotet	939	14	14.1	20	2	S61278	hypothetical prote
867	14	14.1	17	1	A05168	conantokin G [wall	940	14	14.1	20	2	E61497	nikkomycin synthas
868	14	14.1	17	2	S24570	Ig heavy chain J r	941	14	14.1	20	2	S65605	seed protein ws-20
869	14	14.1	17	2	B49404	T-cell receptor be	942	14	14.1	20	2	B60365	dimeric protein (B
870	14	14.1	17	2	B44873	caldesmon - rabbit	943	14	14.1	20	2	S77983	chymotrypsin inhib
871	14	14.1	17	2	A44560	terephthalate 1,2-	944	14	14.1	20	2	A34859	cytochrome-c oxida
872	14	14.1	17	2	S05033	photosystem II pro	945	14	14.1	20	2	PH1326	heliothermiline - Mex
873	14	14.1	17	2	A27636	cyto toxin B - Clo	946	14	14.1	20	2	D49255	Ig heavy chain DJ
874	14	14.1	17	2	C37396	pollen allergen Fe	947	14	14.1	20	2	A49712	T-cell receptor be
875	14	14.1	17	2	A39111	Ig light chain - P	948	14	14.1	20	2	S03954	calcium-dependent
876	14	14.1	17	2	PH1367	Ig heavy chain DJ	949	14	14.1	20	2	I46652	acidic fibroblast
877	14	14.1	17	2	I42753	interferon alpha (950	14	14.1	20	2	A38689	T-cell receptor de
878	14	14.1	17	2	B49255	T-cell receptor be	951	14	14.1	20	2	A42267	I-phosphatidylinos
879	14	14.1	17	2	B31769	T-cell receptor de	952	14	14.1	20	2	PH1352	J-Kappa recombinat
880	14	14.1	17	2	E23734	insulin-like growt	953	14	14.1	20	2	A13050	beta-N-acetylgluco
881	14	14.1	17	2	PH0794	T-cell receptor al	954	14	14.1	20	2	I58192	pyruvate kinase (E
882	14	14.1	17	2	A61019	17k basolateral pl	955	14	14.1	20	2	S66232	glial fibrillary a
883	14	14.1	18	2	F49215	urease (EC 3.5.1.5	956	14	14.1	20	2	A85645	defensin AMP2 - Da
884	14	14.1	18	2	B49215	urease (EC 3.5.1.5	957	14	14.1	20	2	A58903	Amino terminal of
885	14	14.1	18	2	C40433	Nbda protein - Cya	958	14	14.1	20	2	D22565	metalloproteinase
886	14	14.1	18	2	S03528	Ig heavy chain J1	959	14	14.1	21	2	PC2214	R-phycoerythrin be
887	14	14.1	18	2	I52614	u-plasminogen acti	960	14	14.1	21	2	S16073	beta-N-acetylgluco
888	14	14.1	18	2	I51427	hemoglobin alpha c	961	14	14.1	21	2	S47202	alanine-tRNA ligas
889	14	14.1	18	2	C30309	histone H4 - Euplo	962	14	14.1	21	2	PH1730	T-cell receptor J-
890	14	14.1	18	2	S46241	NAD(P)H-flavin oxi	963	14	14.1	21	2	A60420	Ig heavy chain V r
891	14	14.1	18	2	PN0175	glutathione transt	964	14	14.1	21	2	I40157	Iens Intrinsic mem
892	14	14.1	18	2	S70340	napin large chain	965	14	14.1	21	2	S08441	opacity protein P.
893	14	14.1	18	2	S65454	aspargillopepsin I	966	14	14.1	21	2	D48518	tetracycline resis
894	14	14.1	18	2	S63487	fibrinogenolytic p	967	14	14.1	21	2	F64121	rev protein - huma
895	14	14.1	18	2	PT0239	Ig heavy chain CDR	968	14	14.1	21	2	PC7043	PEB1 5'-region hyp
896	14	14.1	18	2	PH1350	Ig heavy chain DJ	969	14	14.1	21	2	S35676	hypothetical prote
897	14	14.1	18	2	S26664	microtubule-assoc	970	14	14.1	21	2	PH1369	ubiquitin carboxyl
898	14	14.1	18	2	S71592	serine proteinase	971	14	14.1	21	2	S58432	Ig heavy chain DJ
899	14	14.1	18	2	PH1815	T cell receptor al	972	14	14.1	22	2	S05057	protein kinase - r
900	14	14.1	18	2	C32537	T-cell receptor al	973	14	14.1	22	2	PT0431	isocitrate dehydro
901	14	14.1	18	2	I46653	T-cell receptor de	974	14	14.1	22	2	A36399	3-methyl-2-oxobuta
902	14	14.1	18	2	PL0025	T-cell surface gly	975	14	14.1	22	2		leucyl aminopeptid
903	14	14.1	19	2	S36120	lectin - Euphorbia	976	14	14.1	22	2		C-type natriuretic
904	14	14.1	19	2	PS0236	trypsin inhibitor	977	14	14.1	22	2		brain natriuretic
905	14	14.1	19	2	S13046	calreticuln - rab	978	14	14.1	22	2	A35418	

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979 14 14.1 22 2 JT0581      natriuretic peptid
980 14 14.1 22 2 I41299      T-cell receptor be
981 14 14.1 22 2 S07966      T-cell receptor be
982 14 14.1 22 2 D32537      T-cell receptor al
983 14 14.1 22 2 S07701      T-cell receptor al
984 14 14.1 22 2 S47206      T-cell receptor J-
985 14 14.1 22 2 H30608      Ig kappa chain V-I
986 14 14.1 22 2 B32711      leghemoglobin - lo
987 14 14.1 22 2 S68616      histone H1 - sea u
988 14 14.1 22 2 C64330      ribosomal protein
989 14 14.1 22 2 PM0048      estrogen receptor
990 14 14.1 22 2 S45058      coat protein - tur
991 14 14.1 22 2 S64675      collagen alpha 3(I
992 14 14.1 22 2 PQ0143      polygalacturonase
993 14 14.1 22 2 PQ0697      hemagglutinin (imp
994 14 14.1 22 2 T25653      hypothetical prote
995 14 14.1 22 2 S65370      tRNA-guanine trans
996 14 14.1 22 2 F84018      hypothetical prote
997 14 14.1 22 2 PC7072      H+-transporting tw
998 14 14.1 23 2 S51188      aldehyde dehydroge
999 14 14.1 23 2 A33105      dihydrofolate redu
1000 14 14.1 23 2 S65379      cytochrome-c oxida

```

ALIGNMENTS

```

RESULT 1
S48654
Plasmeprin II - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jun-2000
C:Accession: S48654
R:Hill, J.; Tyas, L.; Phylip, L.H.; Kay, J.; Dunn, B.M.; Berry, C.
FEBS Lett 352, 155-158, 1994
A:Title: High level expression and characterisation of Plasmeprin II, an aspartic protei
A:Reference number: S48654; MUID:95010698; PMID:7925966
A:Accession: S48654
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-20 <HIL>

```

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Query Match      30.3%; Score 30; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 1 NVGHERMGRG 11      :::|::|::|::|
3 SMTGGQMGMRG 13

```

```

RESULT 2
E39855
paralytic peptide III - beet armyworm
C:Species: Spodoptera exigu (beet armyworm)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: E39855
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
J. Biol. Chem. 266, 12873-12877, 1991
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lepid
A:Reference number: A39855; MUID:91302298; PMID:2071576
A:Accession: E39855
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-23 <SKIT>
C:Superfamily: paralytic peptide I

```

```

Query Match      30.3%; Score 30; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 3 PGHERMGRGR 12      |:::|
11::|

```

```

Db 9 PGYORTADGR 18
RESULT 3
C39855
paralytic peptide I - beet armyworm
C:Species: Spodoptera exigu (beet armyworm)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: C39855
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
J. Biol. Chem. 266, 12873-12877, 1991
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lep
A:Reference number: A39855; MUID:91302298; PMID:2071576
A:Accession: C39855
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-23 <SKIT>
C:Superfamily: paralytic peptide I

```

```

Query Match      30.3%; Score 30; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 3 PGHERMGRGR 12      |:::|
9 PGYORTADGR 18

```

```

RESULT 4
D39855
paralytic peptide II - beet armyworm
C:Species: Spodoptera exigu (beet armyworm)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: D39855
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
J. Biol. Chem. 266, 12873-12877, 1991
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lep
A:Reference number: A39855; MUID:91302298; PMID:2071576
A:Accession: D39855
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-23 <SKIT>
C:Superfamily: paralytic peptide I

```

```

Query Match      30.3%; Score 30; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 3 PGHERMGRGR 12      |:::|
9 PGYORTADGR 18

```

```

RESULT 5
I55453
zinc finger homeodomain protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 15-Oct-1999
C:Accession: I55453
R:Mura, Y.; Tam, T.; Ido, A.; Morinaga, T.; Miki, T.; Hashimoto, T.; Tamaoki, T.
J. Biol. Chem. 270, 26840-26846, 1995
A:Title: Cloning and characterization of an ATBF1 isoform that expresses in a neurona
A:Reference number: I55453; MUID:96070776; PMID:7592926
A:Accession: I55453
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-18 <RES>
A:Cross-references: GB:U32833; NID:9976348; PIDN:AA37582.1; PID:9976349
C:Superfamily: alpha-fetoprotein enhancer-binding protein; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

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Query Match      29.3%; Score 29; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;

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	Matches	6; Conservative	3; Mismatches	3; Indels	0; Gaps	0;
QY	7	RMGRGRTSSNEL	18			
		: :	:			
Db	2	RLGGGLVSEEL	13			

RESULT 6
F39855

Paralytic peptide I - tobacco budworm
 C:Species: *Heliothis virescens* (tobacco budworm)
 C:Date: 30-Dec-1991 #sequence-revision 30-Dec-1991 #text-change 30-Sep-1993
 C:Accession: F39855
 R:Stinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
 J. Biol. Chem. 266, 12873-12877, 1991
 A:Title: Isolation and identification of paralytic peptides from hemolymph of the lepidopteran tobacco budworm, *Heliothis virescens*
 A:Reference number: A39855; MUID:91302298; PMID:2071576
 A:Accession: F39855
 A:Status: preliminary
 A:Molecule type: protein
 Residues: 1-23 <SKT>
 Superfamily: paralytic peptide I

Query Match	29, 3%	Score	29	DB	2	Length	23
Best Local Similarity	45.5%	Pred. No.	3.2e+03				
Matches	5	Conservative	2	Mismatches	4	Indels	0
		Gaps					0
QY	2	VPCHERRGROR	12				
	:	!!!	1				
	:	!!!	1				
DB	8	PGGIMRTADGR	18				

RESULT 7
G39855
paralytic peptide II - tobacco budworm
C:Species: *Heliothis virescens* (tobacco budworm)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: G39855
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
J. Biol. Chem. 266, 12873-12877, 1991
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lepidopteran tobacco budworm, *Heliothis virescens* (Lepidoptera: Noctuidae)
A:Reference number: A39855; MUID:91302298; PMID:2071576
A:Accession: G39855
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <SR>
C:Superfamily: paralytic peptide I

Query Match:	29, 38;	Score 29;	DB 2;	Length 23;
Best Local Similarity:	45.5%;	Pred. No. 3.2e+03;		
Matches	5;	Conservative	2;	Mismatches 4;
				Indels 0;
				Gaps 0;
QY	2	VPGHEHNGRGR	12	
	:	:		
	:	:		
DB	8	IPGYMTADGR	18	

RESULT 8
A31963
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (frax)
C:Species: Ascaris suum (pig roundworm)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 12-Sep-1997
C:Accession: A31963
R:Thissen, J.; Komnietzki, R.
J. Biol. Chem. 263, 19092-19097, 1988
A:Title: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaerob
A:Reference number: A31963; MUID:89066711; PMID:3198613
A:Accession: A31963
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <THI>
C:Keywords: mitochondrion; oxidoreductase; phosphoprotein

Query Match	25.3%	Score 25;	DB 2;	Length 16;
Best Local Similarity	50.0%	Pred. No. 1e+03;		
Matches	6;	Conservative	0;	Mismatches 6; Indels 0; Gaps 0;

QY	4	GHERMGRGRTSS	15
Db	3	GHSSMSDPCGTSS	14

RESULT 9
PL0143
carbon_monoxide_dehydrogenase (EC 1.2.99.2) medium chain - pseudomonas carboxydhydrog
C:Species: Pseudomonas carboxydhydrogena
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C:Accession: PL0143
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydoct
A:Reference number: PL0138; MUID:9005678; PMID:2818128
A:Accession: PL0143
A:Molecule type: protein
A:Residues: 1-15 <KRA>
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large,
C:Keywords: oxidoreductase

Query Match	24.2%	Score 24:	DB 2:	length 15:
Best Local Similarity	75.0%	Pred. No.	1.4e+03:	
Matches	3;	Conservative	1;	Mismatches 0;
				Indels 0;
				Gaps 0
Qy	2	VRGH	5	
		:		
Db	3	lvgH	6	

RESULT 10
PH0766
T-cell receptor beta chain (J3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_rev15n 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0766
R:Caanovaa, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:9207846; PMID:1836010
A:Accession: PH0766
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Cross-references: EMBL:X60860; NID:952745; PIDN:CAA43250.1; PID:952746
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match	24.2%;	Score 24;	DB 2;	Length 16;
Best Local	Similarity 57.1%;	Pred. No. 1.5e+03;		
Matches	4;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0
Ox	10	RGRTSSK	16	
		:		
Db	6	RGRTNER	12	

RESULT 11
C30221 histone H2A.8 - chicken (fragment)
C.Species: Gallus gallus (chicken)
C.Date: 02-Nov-1989 #sequence_revision 02-Nov-1989 #text_change 30-Sep-1993
C.Accession: C30221
R.Challoner, P.B.; Moss, S.B.; Groudine, M.
Mol. Cell. Biol. 9, 902-913, 1989
A.Title: Expression of replication-dependent histone genes in avian spermatids
A.Reference number: A30221; PMID:89261754; PMID:2471062
A.Accession: C30221
A.Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-17 <CHR>

Query Match 24.2%; Score 24; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 9 GRGRTSSKELA 19
|||: | | |
Db 3 GRGKGCKARA 13

RESULT 12

B24735
glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
C:Accession: B24735

R:Mannevik, B.; Alin, P.; Gutheberg, C.; Jansson, H.; Tahlr, M.K.; Warholm, M.; Jorvæ

A:Title: Identification of three classes of cytosolic glutathione transferase common to

A:Reference number: A24735; MUID:86042634; PMID:3864155

A:Accession: B24735

A:Molecule type: protein

A:Residues: 1-18 <MAN>

C:Superfamily: glutathione transferase

C:Keywords: transferase

Query Match 24.2%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

OY 3 PG----HERMGRGR 12
|| | | | | | | | | |
Db 1 PEKPYLHRTNGRGR 14

RESULT 13

S28396

T-complex protein 1 - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Sep-1998

C:Accession: S28396

R:Frydman, J.; Nimmegern, E.; Erdjument-Bromage, H.; Wall, J.S.; Tempst, P.; Hartl, F.U

EMBO J. 11, 4767-4778, 1992

A:Title: Function in protein folding of TRIC, a cytosolic ring complex containing TCP-1

A:Reference number: S28395; MUID:93099850; PMID:1361170

A:Accession: S28396

A:Molecule type: protein

A:Residues: 1-19 <FRY>

C:Superfamily: molecular chaperone t-complex-type

Query Match 24.2%; Score 24; DB 2; Length 19;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 6 ERMGRTSSKELA 19
: | | | | | | | | |
Db 4 DEVGDTSTVTLA 17

RESULT 14

S29858

ribosomal protein S7 - Thermococcus celer (fragment)

C:Species: Thermococcus celer

C:Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 17-Mar-1999

C:Accession: S29858

R:Klenk, H.P.; Schwass, V.; Zillig, W.

Biochim. Biophys. Acta 1172, 236-238, 1993

A:Title: Nucleotide sequence of the genes encoding proline tRNA(UGC) and threonine tRNA(

A:Reference number: S29858; MUID:93176822; PMID:7916630

A:Accession: S29858

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: nucleic acid

A:Residues: 1-21 <KLE>

A:Cross-references: EMBL:X68397

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

Query Match 24.2%; Score 24; DB 2; Length 21;
Best Local Similarity 42.9%; Pred. No. 2e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 6 ERMGRTSSKELA 19
: | | | | | | | | |
Db 7 OQGRDRSDPVL 20

RESULT 15

I50535
calmodulin - electric eel (fragment)

C:Species: Electrophorus electricus (electric eel)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I50535

R:Munjaal, R.P.; Chandra, T.; WOO, S.L.C.; Dedman, J.R.; Means, A.R.

Proc. Natl. Acad. Sci. U.S.A. 78, 2330-2334, 1981

A:Title: A cloned calmodulin structural gene probe is complementary to DNA sequences

A:Reference number: I50535; MUID:81223873; PMID:6941292

A:Accession: I50535

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-21 <MUN>

A:Cross-references: GB:M17495; NID:9213132; PIDN:AAA49237.1; PID:9213133

Query Match 24.2%; Score 24; DB 2; Length 21;
Best Local Similarity 38.5%; Pred. No. 2e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 6 ERMGRTSSKEL 18
: | | | | | | | | |
Db 1 DKEGNGYISAEI 13

RESULT 16

PC4030

rRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)

N:Alternate names: nuclease Ie3

C:Species: Lentinula edodes (shiitake mushroom)

C:Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 20-Mar-1996

C:Accession: PC4030

R:Kobayashi, H.; Inokuchi, N.; Koyama, T.; Tomita, M.; Irie, M.

Biosci. Biotechnol. Biochem. 59, 1169-1171, 1995

A:Title: Purification and characterization of the 2nd 5'-nucleotide-forming nuclease

A:Reference number: PC4030; MUID:95337563; PMID:7613009

A:Accession: PC4030

A:Molecule type: DNA

A:Residues: 1-23 <ROB>

C:Comment: This enzyme has 3'-nucleotidase activity.

C:Keywords: endonuclease; hydrolase

Query Match 24.2%; Score 24; DB 2; Length 23;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 GHERMG 9
| | | | |
Db 5 GHLEVG 10

RESULT 17

S40666

hypothetical protein 2 - wheat dwarf virus

C:Species: wheat dwarf virus

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999

C:Accession: S40666

R:Decker, E.L.; Woolston, C.J.; Xue, Y.; Cox, B.; Mullineaux, P.M.

Nucleic Acids Res. 19, 4075-4081, 1991

A:Title: Transcript mapping reveals different expression strategies for the bicistronic
A:Reference number: S40665; MUID:9133411; PMID:1870964
A:Accession: S40666
A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-24 <DEK>

Query Match 24.2%; Score 24; DB 2; Length 24;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPGH 5
|||
DB 15 IPGH 18

RESULT 18
S78415
ribosomal protein Rl27, mitochondrial [validated] - rat (tentative sequence) (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
Accession: S78415
A:Coltschmidt-Reitsin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A:Reference number: S78411
A:Accession: S78415
A:Molecule type: protein
A:Residues: 1-16 <GOL>

A>Note: 1-Val was also found
A>Note: the protein is designated as mitochondrial ribosomal protein L27
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 23.7%; Score 23.5; DB 2; Length 16;
Best Local Similarity 46.2%; Pred. No. 1.8e+03;
Matches 6; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY 4 GHERMGRRTSK 16
|:|:|:|:
DB 1 GADRMK-RTSKR 12

RESULT 19
JT0610
leukocyte chemoattractant peptide 9 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 19-Jan-2001
C:Accession: JT0610
R:Murdock, W.J.; McCormick, R.J.
Biochem. Biophys. Res. Commun. 184, 848-852, 1992
A:Title: Sequence analysis of leukocyte chemoattractant peptides secreted by peritoneal
A:Reference number: JT0609; MUID:92246975; PMID:1575752
A:Accession: JT0610
A:Molecule type: protein
A:Residues: 1-15 <MOR>
C:Superfamily: unassigned animal peptides

Query Match 23.2%; Score 23; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 VPGHMRGR 10
|:|:|:
DB 5 VAGFGRGR 13

RESULT 20
S36891
ribosomal protein - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36891
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993

A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Myco
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36891
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OHA>

Query Match 23.2%; Score 23; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 NVPGER 7
|||:
DB 4 NVPANSR 10

RESULT 21
CA5143
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 6 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C:Accession: CA5143
R:Yenung, Y.G.; Berg, K.L.; Pixley, F.J.; Angeletti, R.H.; Stanley, E.R.
J. Biol. Chem. 267, 23447-23450, 1992
A:Title: Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine in mac
A:Reference number: A45143; MUID:93054686; PMID:1385421
A:Accession: CA5143
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <YEU>
A:Experimental source: BAC1.2F5 macrophage
A>Note: sequence extracted from NCBI backbone (NCBI:P118515)
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-pho
C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 23.2%; Score 23; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NVPGER 6
|:|:
DB 3 NTPGXD 8

RESULT 22
PS0387
platelet-derived growth factor chain A2 - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-Sep-1993
C:Accession: PS0387
R:Nakahara, K.; Nishimura, H.; Kuro-O, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazak
Biochem. Biophys. Res. Commun. 184, 811-818, 1992
A:Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vas
A:Reference number: JN0248; MUID:92246970; PMID:1575749
A:Accession: PS0387
A:Molecule type: mRNA
A:Residues: 1-18 <NAK>
A>Note: this protein corresponds to the glioma type of human A chain
C:Superfamily: platelet-derived growth factor

Query Match 23.2%; Score 23; DB 2; Length 18;
Best Local Similarity 55.6%; Pred. No. 2.4e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 9 GGRRTSKR 17
|||:
DB 1 GRRRESKK 9

RESULT 23
I50533
calmodulin - electric eel (fragment)
C:Species: Electrophorus electricus (electric eel)

Search completed: March 14, 2003, 16:06:29
Job time : 34 secs

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 29-Sep-1999
C/Accession: 150533
R:Munjal, R.P.; Dedman, J.R.; Means, A.R.
Ann. N. Y. Acad. Sci. 356, 110-118, 1980
A>Title: Isolation of the structural gene for calmodulin.
A/Reference number: 150533; MUID:81205530; PMID:6165309
A/Accession: 150533
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-22 <MUN>
A/Cross-references: GB:M25058; NID:9213127; PIDN:AAA62797.1; PID:9213128
C/Superfamily: calmodulin; calmodulin repeat homology
C/Keywords: EF hand

Query Match 23.2%; Score 23; DB 2; Length 22;
Best Local Similarity 38.5%; Pred. No. 3e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
6 ERNGRGRTSSKEL 18
:: | | | | |
2 DKDNGYISAEL 14

RESULT 24
161239
heparin-binding epidermal growth factor - human (fragment)
C/Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 16-Jul-1999
C/Accession: 161239
R:Ren, Z.; Dhadly, M.S.; Yoshizumi, M.; Hilkert, R.J.; Quettermous, T.; Eddy, R.L.; Show
Biochemistry 32, 7932-7938, 1993
A>Title: Structural organization and chromosomal assignment of the gene encoding the hum
A/Reference number: A5313; MUID:93349877; PMID:8347598
A/Accession: 161239
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-23 <RES>
A/Cross-references: GB:L17031; NID:9348173; PIDN:AAA50564.1; PID:9348174
C/Superfamily: heparin-binding EGF-like growth factor; EGF homology
C/Keywords: heparin binding

Query Match 23.2%; Score 23; DB 2; Length 23;
Best Local Similarity 33.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
1 NYPGHERMGRGRTSS 15
: | | | | |
8 DVNEEKVKLGWMTNS 22

RESULT 25
178886
hypothetical Nf-1 ORF3, E73 protein - mouse (fragment)
C/Species: Mus sp. (mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C/Accession: 178886
R:Nehls, M.; Pfeiffer, D.; Boehm, T.
Oncogene 9, 2169-2175, 1994
A>Title: Exon amplification from complete libraries of genomic DNA using a novel phage v
A/Reference number: 158399; MUID:94309890; PMID:8036002
A/Accession: 178886
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-24 <RES>
A/Cross-references: GB:S71227; NID:9551376; PIDN:AA831327.1; PID:9551377

Query Match 23.2%; Score 23; DB 2; Length 24;
Best Local Similarity 55.6%; Pred. No. 3.2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

7 RMGRGRTSS 15
: | | | | |
9 RIDGNGPSS 17

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:05:03 ; Search time 15 Seconds
(without alignments)
37.269 Million cell updates/sec

Title: US-09-674-913A-1

Perfect score: 99

Sequence: 1 NWGHERMGRGRTSKELA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues 147762

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata2/1aa/PCTus_COMB.pep:*
6: /cgn2_6/prodata2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	99	100.0	25	2	US-08-726-306A-61
2	99	100.0	25	2	US-08-726-306A-87
3	47	47.5	10	2	US-08-726-306A-1
4	33.5	33.8	24	4	US-09-540-224-9
5	32	32.3	16	1	US-08-077-797A-34
6	32	32.3	16	5	PCT-US94-01238-34
7	32	32.3	21	2	US-07-841-591A-11
8	32	32.3	21	5	PCT-US93-02034-11
9	32	32.3	24	2	US-09-047-026A-9
10	31	31.3	14	5	PCT-US93-06751-106
11	31	31.3	16	1	US-07-942-245-142
12	31	31.3	20	4	US-09-166-028-3
13	31	31.3	23	4	US-08-874-569B-14
14	31	31.3	24	2	US-09-047-026A-15
15	30.5	30.8	21	1	US-08-196-945-9
16	30.5	30.8	21	1	US-07-965-667A-10
17	30.5	30.8	21	3	US-08-484-819-10
18	30.5	30.8	21	5	PCT-US93-10197-10
19	30.3	30.3	14	2	US-08-651-818A-20
20	30.3	30.3	14	2	US-08-722-806A-10
21	30	30.3	14	4	US-09-184-826-20
22	30	30.3	14	4	US-09-337-028-10
23	30	30.3	14	4	US-09-597-872-10
24	29	29.3	10	4	US-08-310-912A-95
25	29	29.3	10	4	US-08-841-089-95
26	29	29.3	10	4	US-09-301-085-95
27	29	29.3	10	5	PCT-US95-04570-95

28	29	29.3	10	5	PCT-US95-04589-95	Sequence 95, Appl
29	29	29.3	11	4	US-08-791-113B-17	Sequence 17, Appl
30	29	29.3	14	1	US-08-321-668-29	Sequence 29, Appl
31	29	29.3	14	1	US-08-837-941-29	Sequence 29, Appl
32	29	29.3	16	1	US-07-942-245-143	Sequence 143, App
33	29	29.3	17	4	US-09-297-981-23	Sequence 23, Appl
34	29	29.3	18	2	US-08-859-201-10	Sequence 10, Appl
35	29	29.3	23	2	US-08-609-443B-22	Sequence 22, Appl
36	29	29.3	23	2	US-08-569-063C-19	Sequence 19, Appl
37	29	29.3	23	4	US-08-851-896-22	Sequence 22, Appl
38	29	29.3	24	2	US-08-706-741B-32	Sequence 32, Appl
39	29	29.3	24	2	US-09-047-026A-11	Sequence 11, Appl
40	29	29.3	24	2	US-09-047-026A-13	Sequence 13, Appl
41	29	29.3	24	2	US-08-924-692A-32	Sequence 32, Appl
42	28.5	28.8	25	4	US-08-469-526A-242	Sequence 24, App
43	28	28.3	14	4	US-09-297-981-26	Sequence 26, Appl
44	28	28.3	16	1	US-07-942-245-140	Sequence 140, App
45	28	28.3	20	4	US-08-895-590-20	Sequence 20, Appl
46	27	27.3	10	1	US-08-445-745-106	Sequence 106, App
47	27	27.3	10	4	US-08-456-466-84	Sequence 84, Appl
48	27	27.3	11	4	US-09-133-062D-26	Sequence 26, Appl
49	27	27.3	15	2	US-08-310-912A-73	Sequence 73, Appl
50	27	27.3	15	3	US-08-841-089-73	Sequence 73, Appl
51	27	27.3	15	4	US-09-301-085-73	Sequence 73, Appl
52	27	27.3	15	5	PCT-US93-06751-71	Sequence 71, Appl
53	27	27.3	15	5	PCT-US95-04570-73	Sequence 73, Appl
54	27	27.3	15	5	PCT-US95-04589-73	Sequence 73, Appl
55	27	27.3	16	1	US-08-068-946A-1	Sequence 1, Appl1
56	27	27.3	16	1	US-08-456-221-1	Sequence 1, Appl1
57	27	27.3	16	2	US-08-373-190-8	Sequence 8, Appl1
58	27	27.3	16	2	US-08-438-190A-8	Sequence 8, Appl1
59	27	27.3	16	3	US-08-350-215-8	Sequence 8, Appl1
60	27	27.3	16	3	US-09-287-145A-8	Sequence 8, Appl1
61	27	27.3	16	4	US-09-556-111-8	Sequence 8, Appl1
62	27	27.3	16	4	US-08-443-888-1	Sequence 1, Appl1
63	27	27.3	24	2	US-08-146-028-69	Sequence 69, Appl
64	27	27.3	24	4	US-08-723-425A-69	Sequence 69, Appl
65	27	27.3	24	4	US-09-112-206-69	Sequence 69, Appl
66	27	27.3	25	4	US-09-292-225-23	Sequence 23, Appl
67	26	26.3	11	1	US-08-476-405A-15	Sequence 15, Appl
68	26	26.3	12	1	US-08-033-857A-2	Sequence 2, Appl1
69	26	26.3	12	1	US-08-374-983A-2	Sequence 2, Appl1
70	26	26.3	12	2	US-08-260-582-53	Sequence 53, Appl
71	26	26.3	12	5	PCT-US95-05471-53	Sequence 53, Appl
72	26	26.3	13	1	US-07-781-254A-82	Sequence 82, Appl
73	26	26.3	14	1	US-08-471-780C-85	Sequence 85, Appl
74	26	26.3	14	1	US-08-467-282B-85	Sequence 85, Appl
75	26	26.3	14	2	US-08-471-282A-85	Sequence 85, Appl
76	26	26.3	14	2	US-08-466-710C-85	Sequence 85, Appl
77	26	26.3	14	3	US-08-468-739C-85	Sequence 85, Appl
78	26	26.3	16	1	US-08-287-717-12	Sequence 12, Appl
79	26	26.3	16	1	US-07-942-245-141	Sequence 141, App
80	26	26.3	16	1	US-08-441-914-12	Sequence 12, Appl
81	26	26.3	18	4	US-09-297-981-21	Sequence 21, Appl
82	26	26.3	19	1	US-08-287-717-11	Sequence 11, Appl
83	26	26.3	19	1	US-08-441-914-11	Sequence 11, Appl
84	26	26.3	19	4	US-08-827-962-2	Sequence 2, Appl
85	26	26.3	19	6	5266328-2	Patent No. 5266328
86	26	26.3	20	1	US-08-279-906A-21	Sequence 21, Appl
87	26	26.3	20	1	US-09-166-028-4	Sequence 4, Appl1
88	26	26.3	20	4	US-09-166-028-5	Sequence 5, Appl1
89	26	26.3	21	4	US-07-847-743B-4	Sequence 4, Appl1
90	26	26.3	21	1	US-08-036-555B-30	Sequence 30, Appl
91	26	26.3	21	1	US-08-469-569-30	Sequence 30, Appl
92	26	26.3	21	1	US-08-456-201-4	Sequence 4, Appl1
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94	26	26.3	21	1	US-08-249-322A-30	Sequence 30, Appl
95	26	26.3	21	1	US-08-469-562A-30	Sequence 30, Appl
96	26	26.3	21	2	US-08-330-161-4	Sequence 4, Appl1
97	26	26.3	21	2	US-08-456-241-4	Sequence 4, Appl1
98	26	26.3	21	2	US-08-734-551A-30	Sequence 30, Appl
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102	26	26.3	21	4	US-08-470-335-30	Sequence 30, App1	175	24.5	24.7	8	5	PCT-US93-10197-1	Sequence 2, App1
103	26	26.3	21	4	US-08-735-021-30	Sequence 30, App1	176	24	24.2	21	1	US-08-153-855-2	Sequence 1, App1
104	26	26.3	21	4	US-08-734-664A-30	Sequence 30, App1	177	24	24.2	9	2	US-08-726-064-7	Sequence 7, App1
105	26	26.3	21	4	US-08-470-339-30	Sequence 30, App1	178	24	24.2	10	1	US-08-445-745-103	Sequence 103, App
106	26	26.3	21	4	US-09-173-480-4	Sequence 4, App1	179	24	24.2	10	1	US-08-445-745-105	Sequence 105, App
107	26	26.3	21	4	US-08-467-602-30	Sequence 30, App1	180	24	24.2	10	1	US-08-445-745-110	Sequence 110, App
108	26	26.3	21	5	PCT-US92-04295A-4	Sequence 4, App1	181	24	24.2	10	1	US-08-445-745-117	Sequence 117, App
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111	26	26.3	22	1	US-08-287-717-10	Sequence 10, App1	184	24	24.2	10	3	US-09-139-762A-102	Sequence 102, App
112	26	26.3	22	1	US-08-441-914-10	Sequence 10, App1	185	24	24.2	10	4	US-09-074-658-57	Sequence 57, App1
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114	26	26.3	23	6	5225193-10	Patent No. 5225193	187	24	24.2	10	4	US-08-456-466-83	Sequence 83, App1
115	26	26.3	24	2	US-08-146-028-75	Sequence 75, App1	188	24	24.2	10	4	US-08-456-466-95	Sequence 95, App1
116	26	26.3	24	4	US-08-723-425A-75	Sequence 75, App1	189	24	24.2	11	4	US-08-039-778B-6	Sequence 3, App1
117	26	26.3	24	4	US-09-112-206-75	Sequence 75, App1	190	24	24.2	11	1	US-08-039-778B-6	Sequence 6, App1
118	26	26.3	24	4	US-08-112-206-75	Sequence 75, App1	191	24	24.2	11	1	US-08-469-582-19	Sequence 19, App1
119	26	26.3	25	1	US-08-798-897-21	Sequence 21, App1	192	24	24.2	11	2	US-08-473-025-12	Sequence 12, App1
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122	25	25.3	7	1	US-07-634-641-14	Sequence 14, App1	195	24	24.2	11	4	US-09-299-495F-51	Sequence 51, App1
123	25	25.3	11	1	US-08-469-582-7	Sequence 7, App1	196	24	24.2	11	4	US-08-196-898B-7	Sequence 7, App1
124	25	25.3	11	2	US-08-669-721-20	Sequence 20, App1	197	24	24.2	12	1	US-08-260-882-60	Sequence 60, App1
125	25	25.3	11	2	US-08-350-260A-484	Sequence 84, App	198	24	24.2	12	1	US-08-260-882-60	Sequence 60, App1
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127	25	25.3	11	3	US-08-542-051-8	Sequence 8, App1	200	24	24.2	12	2	US-09-579-181-3	Sequence 3, App1
128	25	25.3	11	3	US-08-642-246-35	Sequence 35, App1	201	24	24.2	12	4	US-08-469-260A-501	Sequence 501, App
129	25	25.3	11	4	US-09-189-344-20	Sequence 20, App1	202	24	24.2	12	4	PCT-US95-05471-60	Sequence 60, App1
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132	25	25.3	11	5	PCT-US96-06229-35	Sequence 35, App1	205	24	24.2	13	4	US-09-289-495F-33	Sequence 33, App1
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134	25	25.3	12	2	US-08-473-025-13	Sequence 13, App1	207	24	24.2	14	4	US-09-261-855-5	Sequence 5, App1
135	25	25.3	12	4	US-08-817-441-26	Sequence 26, App1	208	24	24.2	14	4	US-08-687-590-35	Sequence 35, App1
136	25	25.3	13	1	US-07-781-254A-19	Sequence 19, App1	209	24	24.2	14	4	US-08-687-590-36	Sequence 36, App1
137	25	25.3	14	1	US-08-469-582-4	Sequence 4, App1	210	24	24.2	14	4	US-08-182-967-21	Sequence 24, App1
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139	25	25.3	15	4	US-09-009-953-107	Sequence 107, App	212	24	24.2	14	5	PCT-US93-06751-105	Sequence 105, App
140	25	25.3	15	4	US-09-009-953-117	Sequence 117, App	213	24	24.2	15	5	PCT-US93-06751-110	Sequence 110, App
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142	25	25.3	16	2	US-08-124-981A-27	Sequence 27, App1	215	24	24.2	15	1	US-08-254-359A-29	Sequence 29, App1
143	25	25.3	16	3	US-09-037-190-25	Sequence 25, App1	216	24	24.2	15	1	US-08-483-043-29	Sequence 29, App1
144	25	25.3	16	3	US-09-037-192-25	Sequence 25, App1	217	24	24.2	15	1	US-08-481-238-29	Sequence 29, App1
145	25	25.3	16	4	US-09-037-143-25	Sequence 25, App1	218	24	24.2	15	2	US-08-471-066B-29	Sequence 29, App1
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160	25	25.3	20	4	US-09-556-877-248	Sequence 248, App	233	24	24.2	16	1	US-08-373-190-7	Sequence 7, App1
161	25	25.3	20	4	US-09-620-412C-248	Sequence 248, App	234	24	24.2	18	2	US-08-373-190-7	Sequence 7, App1
162	25	25.3	20	4	US-09-620-412C-247	Sequence 247, App	235	24	24.2	18	2	US-08-373-190-7	Sequence 7, App1
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165	25	25.3	23	1	US-07-811-048-8	Sequence 8, App1	238	24	24.2	18	2	US-08-438-190A-7	Sequence 7, App1
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171	25	25.3	25	5	US-08-248-839C-107	Sequence 107, App	244	24	24.2	18	5	PCT-US93-06751-137	Sequence 7, App1
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			21	1	US-07-965-667A-1	Sequence 1, App1							

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253	24	24.2	20	2	US-08-542-927-6	Sequence 6, Appl	326	23	23.2	15	4	US-08-370-476-30	Sequence 30, Appl
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258	24	24.2	22	1	US-08-039-778B-2	Sequence 2, Appl	331	23	23.2	15	4	US-09-503-632-4	Sequence 4, Appl
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261	24	24.2	22	4	US-09-556-877-218	Sequence 218, App	334	23	23.2	16	1	US-07-942-245-66	Sequence 66, Appl
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263	24	24.2	22	6	5182262-10	Patent No. 5182262	336	23	23.2	16	1	US-07-942-245-18	Sequence 18, App
264	24	24.2	22	6	5182262-10	Patent No. 5182262	337	23	23.2	16	1	US-07-942-245-18	Sequence 18, App
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267	24	24.2	23	1	US-08-176-500-89	Sequence 89, Appl	340	23	23.2	17	4	US-08-469-260A-179	Sequence 179, App
268	24	24.2	23	1	US-08-471-052A-89	Sequence 89, Appl	341	23	23.2	17	4	US-08-381-601-2	Sequence 2, Appl
269	24	24.2	23	1	US-08-189-331-89	Sequence 89, Appl	342	23	23.2	18	1	US-08-468-674B-13	Sequence 13, Appl
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271	24	24.2	23	2	US-08-471-800-89	Sequence 89, Appl	344	23	23.2	18	1	US-08-634-060-54	Sequence 54, Appl
272	24	24.2	23	2	US-08-471-068-89	Sequence 89, Appl	345	23	23.2	18	1	US-08-780-571-13	Sequence 13, Appl
273	24	24.2	23	4	US-09-297-981-19	Sequence 19, Appl	346	23	23.2	18	2	US-08-685-589A-214	Sequence 214, App
274	24	24.2	24	4	US-09-028-937-12	Sequence 12, Appl	347	23	23.2	18	2	US-08-476-866-22	Sequence 22, Appl
275	24	24.2	24	4	US-09-206-942-4	Sequence 4, Appl	348	23	23.2	18	4	US-09-467-997-9	Sequence 9, Appl
276	24	24.2	25	2	US-08-146-028-17	Sequence 17, Appl	349	23	23.2	18	4	US-08-469-260A-302	Sequence 302, App
277	24	24.2	25	2	US-08-146-028-17	Sequence 17, Appl	350	23	23.2	18	5	PCF-US93-05325-12	Sequence 12, Appl
278	24	24.2	25	2	US-08-192-553-25	Sequence 25, Appl	351	23	23.2	18	5	PCF-US93-06751-139	Sequence 139, App
279	24	24.2	25	4	US-08-723-425A-17	Sequence 17, Appl	352	23	23.2	19	5	PCF-US94-02631-33	Sequence 33, Appl
280	24	24.2	25	4	US-08-723-425A-163	Sequence 163, App	353	23	23.2	19	5	US-08-347-000-15	Sequence 10, Appl
281	24	24.2	25	4	US-09-112-206-17	Sequence 17, Appl	354	23	23.2	19	4	US-09-169-015-52	Sequence 52, Appl
282	24	24.2	25	4	US-09-112-206-163	Sequence 163, App	355	23	23.2	19	4	US-09-381-601-1	Sequence 1, Appl
283	24	24.2	25	4	US-09-381-601-6	Sequence 6, Appl	356	23	23.2	19	4	US-08-871-561-39	Sequence 39, Appl
284	23	23.7	16	4	US-09-227-357-520	Sequence 24, Appl	357	23	23.2	19	4	US-09-321-932B-39	Sequence 9, Appl
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287	23	23.2	10	2	US-08-406-330-18	Sequence 18, Appl	360	23	23.2	20	1	US-07-700-526-15	Sequence 15, Appl
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293	23	23.2	10	3	US-08-482-528-202	Sequence 202, App	366	23	23.2	20	4	US-09-556-877-249	Sequence 249, App
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297	23	23.2	12	1	US-08-260-582-45	Sequence 45, Appl	370	23	23.2	20	5	PCF-US93-05325-11	Sequence 11, Appl
298	23	23.2	12	1	US-08-260-582-56	Sequence 56, Appl	371	23	23.2	20	5	PCF-US93-05325-11	Sequence 11, Appl
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306	23	23.2	12	5	PCF-US95-05471-45	Sequence 45, Appl	379	23	23.2	22	2	US-08-896-716-3	Sequence 3, Appl
307	23	23.2	12	5	PCF-US95-05471-45	Sequence 45, Appl	380	23	23.2	22	2	US-09-130-225-53	Sequence 53, Appl
308	23	23.2	12	5	PCF-US95-05471-45	Sequence 45, Appl	381	23	23.2	22	4	US-09-435-061-53	Sequence 53, Appl
309	23	23.2	12	6	546668-10	Patent No. 546668	382	23	23.2	23	2	US-08-850-910A-27	Sequence 27, Appl
310	23	23.2	13	4	US-08-444-818-129	Sequence 129, App	383	23	23.2	23	2	US-07-748-344B-3	Sequence 3, Appl
311	23	23.2	13	4	US-09-206-059-25	Sequence 25, Appl	384	23	23.2	24	1	US-08-657-152-10	Sequence 10, Appl
312	23	23.2	13	6	5166321-6	Patent No. 5166321	385	23	23.2	24	2	US-08-465-794-1	Sequence 1, Appl
313	23	23.2	14	3	US-08-637-759B-214	Sequence 214, App	386	23	23.2	24	2	US-08-954-965A-3	Sequence 3, Appl
314	23	23.2	14	3	US-08-871-335A-214	Sequence 214, App	387	23	23.2	24	2	US-09-047-026A-8	Sequence 8, Appl
315	23	23.2	14	4	US-08-433-613-15	Sequence 15, Appl	388	23	23.2	24	3	US-09-049-813-1	Sequence 1, Appl
316	23	23.2	14	4	US-09-248-574A-1	Sequence 1, Appl	389	23	23.2	24	3	US-08-256-747C-67	Sequence 67, Appl
317	23	23.2	14	4	US-09-201-945-214	Sequence 214, App	390	23	23.2	24	3	US-08-834-130A-67	Sequence 67, Appl
318	23	23.2	14	4	US-09-248-574A-1	Sequence 1, Appl	391	23	23.2	24	4		
319	23	23.2	14	4	US-09-929-962-1	Sequence 1, Appl	392	23	23.2	24	4		

393	23	23.2	24	4	US-09-400-208B-3	Sequence 3, Appl1	466	22	22.2	15	2	US-08-733-982A-14	Sequence 14, Appl1
394	23	23.2	24	6	US-08-137-086-3	Sequence 3, Appl1	467	22	22.2	15	2	US-08-933-402-122	Sequence 122, App
395	23	23.2	24	6	5171680-13	Patent No. 5171680	468	22	22.2	15	2	US-09-207-621-122	Sequence 122, App
396	23	23.2	25	1	US-07-748-344B-1	Sequence 1, Appl1	469	22	22.2	15	2	US-08-532-818-122	Sequence 122, App
397	23	23.2	25	2	US-08-621-564B-2	Sequence 2, Appl1	470	22	22.2	15	2	US-08-752-852A-119	Sequence 119, App
398	23	23.2	25	2	US-08-473-475A-6	Sequence 6, Appl1	471	22	22.2	15	3	US-08-934-224-122	Sequence 122, App
399	23	23.2	25	2	US-08-997-080-64	Sequence 64, Appl1	472	22	22.2	15	3	US-08-933-843-122	Sequence 122, App
400	23	23.2	25	2	US-08-954-985A-1	Sequence 1, Appl1	473	22	22.2	15	3	US-08-469-141A-11	Sequence 11, Appl
401	23	23.2	25	2	US-08-997-362-64	Sequence 64, Appl1	474	22	22.2	15	3	US-08-934-223-122	Sequence 122, App
402	23	23.2	25	3	US-08-873-970-64	Sequence 64, Appl1	475	22	22.2	15	4	US-08-706-391A-8	Sequence 8, Appl1
403	23	23.2	25	3	US-09-095-855-64	Sequence 64, Appl1	476	22	22.2	15	4	US-08-602-999A-345	Sequence 345, App
404	23	23.2	25	4	US-09-381-601-5	Sequence 5, Appl1	477	22	22.2	15	4	US-09-413-492-122	Sequence 122, App
405	23	23.2	25	4	US-09-324-542-64	Sequence 64, Appl1	478	22	22.2	15	4	US-08-997-251-6	Sequence 6, Appl1
406	23	23.2	25	4	US-09-205-426-64	Sequence 64, Appl1	479	22	22.2	15	4	US-08-630-915A-171	Sequence 171, App
407	23	23.2	25	4	US-08-137-086-1	Sequence 1, Appl1	480	22	22.2	15	4	US-09-500-124-345	Sequence 345, App
408	22.5	22.7	13	1	US-08-184-184-3	Sequence 3, Appl1	481	22	22.2	15	4	US-09-561-490E-9	Sequence 9, Appl1
409	22.5	22.7	13	1	US-08-087-219-3	Sequence 3, Appl1	482	22	22.2	15	4	PCT-US93-06751-6	Sequence 6, Appl1
410	22.5	22.7	13	1	US-08-269-929-7	Sequence 7, Appl1	483	22	22.2	15	5	PCT-US93-06751-7	Sequence 7, Appl1
411	22.5	22.7	16	4	US-09-297-981-28	Sequence 28, Appl1	484	22	22.2	15	5	PCT-US93-06751-32	Sequence 32, Appl1
412	22.5	22.7	19	4	US-09-106-568B-91	Sequence 91, Appl1	485	22	22.2	15	5	PCT-US93-06751-52	Sequence 52, Appl1
413	22.5	22.7	22	1	US-09-698-928A-5	Sequence 5, Appl1	486	22	22.2	15	5	PCT-US93-06751-86	Sequence 86, Appl1
414	22.5	22.7	22	4	US-09-127-815D-36	Sequence 36, Appl1	487	22	22.2	15	5	PCT-US95-13794-11	Sequence 11, Appl1
415	22.2	22.2	5	3	US-08-985-526-17	Sequence 17, Appl1	488	22	22.2	15	5	US-08-447-925-5	Sequence 5, Appl1
416	22	22.2	5	4	US-08-290-995-3	Sequence 3, Appl1	489	22	22.2	16	1	US-07-942-245-65	Sequence 65, Appl1
417	22	22.2	5	4	US-08-264-002-13	Sequence 13, Appl1	490	22	22.2	16	1	US-07-942-245-70	Sequence 70, Appl1
418	22	22.2	8	4	US-08-635-928-15	Sequence 15, Appl1	491	22	22.2	16	1	US-07-942-245-99	Sequence 99, Appl1
419	22	22.2	8	4	US-08-817-441-24	Sequence 24, Appl1	492	22	22.2	16	1	US-07-942-245-103	Sequence 103, App
420	22	22.2	8	6	5204259-20	Patent No. 5204259	493	22	22.2	16	1	US-07-942-245-104	Sequence 104, App
421	22	22.2	9	1	US-08-454-207A-70	Sequence 70, Appl1	494	22	22.2	16	1	US-07-942-245-113	Sequence 113, App
422	22	22.2	9	1	US-08-615-181-90	Sequence 90, Appl1	495	22	22.2	16	1	US-08-257-528B-73	Sequence 73, App
423	22	22.2	9	2	US-08-704-655-24	Sequence 24, Appl1	496	22	22.2	16	1	US-08-182-483A-20	Sequence 20, Appl1
424	22	22.2	9	3	US-09-162-368B-24	Sequence 24, Appl1	497	22	22.2	16	1	US-08-243-879A-13	Sequence 13, Appl1
425	22	22.2	9	4	US-09-161-877B-24	Sequence 24, Appl1	498	22	22.2	16	1	US-08-460-602A-73	Sequence 73, Appl1
426	22	22.2	9	4	US-09-675-922-27	Sequence 27, Appl1	499	22	22.2	16	1	US-08-463-966A-73	Sequence 73, Appl1
427	22	22.2	10	1	US-08-300-386A-56	Sequence 56, Appl1	500	22	22.2	16	1	US-08-465-217A-73	Sequence 73, Appl1
428	22	22.2	10	2	US-09-016-366A-56	Sequence 56, Appl1	501	22	22.2	16	1	US-08-499-523-40	Sequence 40, Appl1
429	22	22.2	10	2	US-08-978-404B-35	Sequence 35, Appl1	502	22	22.2	16	1	US-08-464-329A-73	Sequence 73, Appl1
430	22	22.2	10	3	US-08-159-339A-669	Sequence 669, Appl1	503	22	22.2	16	2	US-08-615-942A-9	Sequence 9, Appl1
431	22	22.2	10	3	US-08-931-645-56	Sequence 56, Appl1	504	22	22.2	16	2	US-08-462-507A-73	Sequence 73, Appl1
432	22	22.2	10	4	US-09-330-548-5	Sequence 5, Appl1	505	22	22.2	16	2	US-08-467-881A-73	Sequence 73, Appl1
433	22	22.2	10	5	PCT-US94-01258-56	Sequence 56, Appl1	506	22	22.2	16	2	US-09-128-345-40	Sequence 40, Appl1
434	22	22.2	10	5	PCT-US95-11235-56	Sequence 56, Appl1	507	22	22.2	16	4	US-09-128-345-40	Sequence 40, Appl1
435	22	22.2	10	6	5204259-11	Patent No. 5204259	508	22	22.2	16	4	US-08-602-999A-211	Sequence 211, App
436	22	22.2	11	2	US-08-669-721-16	Sequence 16, Appl1	509	22	22.2	16	4	US-09-488-799-5	Sequence 5, Appl1
437	22	22.2	11	3	US-09-075-257A-19	Sequence 19, Appl1	510	22	22.2	16	4	US-09-230-548-17	Sequence 17, Appl1
438	22	22.2	11	4	US-08-836-075A-116	Sequence 116, Appl1	511	22	22.2	16	4	US-09-500-124-211	Sequence 211, App
439	22	22.2	11	4	US-09-189-344-16	Sequence 16, Appl1	512	22	22.2	17	2	US-09-115-209-69	Sequence 69, Appl1
440	22	22.2	11	4	US-09-534-639-19	Sequence 19, Appl1	513	22	22.2	17	4	US-08-990-823-101	Sequence 101, App
441	22	22.2	11	4	US-09-297-981-18	Sequence 18, Appl1	514	22	22.2	18	1	US-08-061-350-4	Sequence 1, Appl1
442	22	22.2	11	6	5223254-12	Patent No. 5223254	515	22	22.2	18	1	US-08-553-110-1	Sequence 1, Appl1
443	22	22.2	12	1	US-07-854-629-7	Sequence 7, Appl1	516	22	22.2	18	2	US-08-224-591-10	Sequence 10, Appl1
444	22	22.2	12	1	US-08-474-008-7	Sequence 7, Appl1	517	22	22.2	18	2	US-08-819-033-3	Sequence 3, Appl1
445	22	22.2	12	2	US-08-811-492-134	Sequence 134, Appl1	518	22	22.2	18	2	US-08-649-991-51	Sequence 51, Appl1
446	22	22.2	12	2	US-08-564-972-73	Sequence 73, Appl1	519	22	22.2	18	2	US-08-926-789-10	Sequence 10, Appl1
447	22	22.2	12	3	US-08-816-346-34	Sequence 34, Appl1	520	22	22.2	18	2	US-08-818-253-45	Sequence 45, Appl1
448	22	22.2	12	4	US-09-335-411-34	Sequence 34, Appl1	521	22	22.2	18	3	US-08-946-026-50	Sequence 50, Appl1
449	22	22.2	12	4	US-09-258-734-95	Sequence 95, Appl1	522	22	22.2	18	4	US-09-070-637-13	Sequence 13, Appl1
450	22	22.2	12	4	US-09-042-107-95	Sequence 95, Appl1	523	22	22.2	18	4	US-08-818-252-45	Sequence 45, Appl1
451	22	22.2	12	4	US-09-518-046-34	Sequence 34, Appl1	524	22	22.2	18	4	US-09-362-805-7	Sequence 7, Appl1
452	22	22.2	12	4	US-09-297-981-30	Sequence 30, Appl1	525	22	22.2	18	4	US-09-173-190-7	Sequence 7, Appl1
453	22	22.2	14	1	US-08-471-780C-89	Sequence 89, Appl1	526	22	22.2	18	4	US-09-069-821-10	Sequence 10, Appl1
454	22	22.2	14	1	US-08-467-282B-89	Sequence 89, Appl1	527	22	22.2	18	4	US-09-316-919-61	Sequence 61, Appl1
455	22	22.2	14	2	US-08-471-282A-89	Sequence 89, Appl1	528	22	22.2	18	5	PCT-US93-11138-10	Sequence 10, Appl1
456	22	22.2	14	2	US-08-466-710C-89	Sequence 89, Appl1	529	22	22.2	18	5	PCT-US94-01234-9	Sequence 9, Appl1
457	22	22.2	14	3	US-08-468-739C-89	Sequence 89, Appl1	530	22	22.2	19	1	US-08-492-599-3	Sequence 3, Appl1
458	22	22.2	14	4	US-08-687-590-44	Sequence 44, Appl1	531	22	22.2	19	1	US-08-975-699-16	Sequence 16, Appl1
459	22	22.2	14	4	US-08-687-590-47	Sequence 44, Appl1	532	22	22.2	19	2	US-08-972-089-16	Sequence 16, Appl1
460	22	22.2	14	5	PCT-US93-06751-74	Sequence 74, Appl1	533	22	22.2	19	4	US-09-166-028-1	Sequence 1, Appl1
461	22	22.2	14	5	PCT-US93-06751-77	Sequence 77, Appl1	534	22	22.2	19	4	US-08-628-829-23	Sequence 23, Appl1
462	22	22.2	15	1	US-07-805-437-8	Sequence 8, Appl1	535	22	22.2	19	4	US-09-297-981-16	Sequence 16, Appl1
463	22	22.2	15	1	US-07-969-336-1	Sequence 1, Appl1	536	22	22.2	19	4	US-09-210-422-15	Sequence 15, Appl1
464	22	22.2	15	2	US-08-815-953-1	Sequence 122, App	537	22	22.2	19	5	PCT-US96-10455-2	Sequence 2, Appl1
465	22	22.2	15	2	US-08-934-222-122	Sequence 122, App	538	22	22.2	19	5		

539	22	22.2	19	5	PCT-US96-10455-3	Sequence 3, Appl	612	21	21.2	7	4	US-09-173-941-10	Sequence 10, Appl
540	22	22.2	20	1	US-08-066-309-3	Sequence 3, Appl	613	21	21.2	7	4	US-09-173-941-61	Sequence 61, Appl
541	22	22.2	20	1	US-08-218-608-7	Sequence 7, Appl	614	21	21.2	7	4	US-09-173-941-63	Sequence 63, Appl
542	22	22.2	20	2	US-08-564-972-43	Sequence 43, Appl	615	21	21.2	7	4	US-09-173-941-73	Sequence 73, Appl
543	22	22.2	20	2	US-08-564-972-44	Sequence 44, Appl	616	21	21.2	7	4	US-08-640-737-35	Sequence 35, Appl
544	22	22.2	20	2	US-08-240-717A-2	Sequence 2, Appl	617	21	21.2	8	2	US-08-318-837-30	Sequence 30, Appl
545	22	22.2	20	3	US-08-504-538A-3	Sequence 3, Appl	618	21	21.2	8	2	US-08-810-712-19	Sequence 19, Appl
546	22	22.2	20	4	US-08-861-338-4	Sequence 4, Appl	619	21	21.2	8	6	5175147-10	Patent No. 5175147
547	22	22.2	20	4	US-08-160-604-127	Sequence 127, App	620	21	21.2	9	1	US-08-469-582-14	Sequence 14, Appl
548	22	22.2	20	4	US-08-249-458A-3	Sequence 3, Appl	621	21	21.2	9	1	US-08-615-181-46	Sequence 46, Appl
549	22	22.2	20	4	US-08-290-736C-45	Sequence 45, Appl	622	21	21.2	9	2	US-08-704-655-23	Sequence 23, Appl
550	22	22.2	20	4	US-08-630-052-3	Sequence 3, Appl	623	21	21.2	9	4	US-09-644-600-62	Sequence 62, Appl
551	22	22.2	20	4	US-09-556-877-246	Sequence 246, App	624	21	21.2	10	1	US-08-445-745-52	Sequence 52, Appl
552	22	22.2	20	4	US-09-620-412C-246	Sequence 246, App	625	21	21.2	10	1	US-08-445-745-58	Sequence 58, Appl
553	22	22.2	20	5	PCT-US94-05660-3	Sequence 3, Appl	626	21	21.2	10	1	US-08-445-745-104	Sequence 104, App
554	22	22.2	20	5	PCT-US95-09307-3	Sequence 3, Appl	627	21	21.2	10	1	US-08-445-745-107	Sequence 107, App
555	22	22.2	21	1	US-08-127-499A-2	Sequence 2, Appl	628	21	21.2	10	1	US-08-445-745-108	Sequence 108, App
556	22	22.2	21	1	US-08-482-847-2	Sequence 2, Appl	629	21	21.2	10	1	US-08-469-582-11	Sequence 11, Appl
557	22	22.2	21	2	US-08-480-190-272	Sequence 272, App	630	21	21.2	10	1	US-08-704-170-27	Sequence 27, Appl
558	22	22.2	21	2	US-08-488-379-272	Sequence 272, App	631	21	21.2	10	1	US-08-218-026-13	Sequence 66, Appl
559	22	22.2	21	2	US-08-485-937-7	Sequence 7, Appl	632	21	21.2	10	1	US-08-218-026-15	Sequence 13, Appl
560	22	22.2	21	2	US-08-373-215-7	Sequence 7, Appl	633	21	21.2	10	2	US-08-653-632-13	Sequence 13, Appl
561	22	22.2	21	4	US-09-057-897-31	Sequence 31, Appl	634	21	21.2	10	2	US-08-653-632-15	Sequence 15, Appl
562	22	22.2	21	5	PCT-US93-06552-7	Sequence 7, Appl	635	21	21.2	10	2	US-08-556-597-134	Sequence 134, App
563	22	22.2	21	5	PCT-US93-07545-272	Sequence 7, App	636	21	21.2	10	2	US-08-556-597-172	Sequence 172, App
564	22	22.2	22	1	US-08-678-444-1	Sequence 1, Appl	637	21	21.2	10	2	US-08-769-745-3	Sequence 3, Appl
565	22	22.2	22	1	US-08-484-635-174	Sequence 174, App	638	21	21.2	10	3	US-08-997-5328-2	Sequence 2, Appl
566	22	22.2	22	2	US-08-484-631-174	Sequence 174, App	639	21	21.2	10	4	US-09-306-756-1	Sequence 1, Appl
567	22	22.2	22	2	US-08-248-839C-73	Sequence 73, App	640	21	21.2	10	4	US-09-194-062-12	Sequence 12, Appl
568	22	22.2	22	2	US-08-827-570-174	Sequence 174, App	641	21	21.2	10	4	US-08-456-466-1	Sequence 1, Appl
569	22	22.2	22	2	US-08-751-767A-78	Sequence 78, App	642	21	21.2	10	4	US-08-456-466-28	Sequence 28, Appl
570	22	22.2	22	2	US-08-985-526-19	Sequence 19, Appl	643	21	21.2	10	4	US-08-456-466-35	Sequence 35, Appl
571	22	22.2	22	3	US-09-100-409A-52	Sequence 52, Appl	644	21	21.2	10	4	US-08-456-466-82	Sequence 82, Appl
572	22	22.2	22	3	US-08-469-260A-558	Sequence 558, App	645	21	21.2	10	4	US-08-456-466-85	Sequence 85, Appl
573	22	22.2	22	5	PCT-US92-08094-6	Sequence 6, Appl	646	21	21.2	10	4	US-08-456-466-86	Sequence 86, Appl
574	22	22.2	23	1	US-08-112-208C-21	Sequence 21, Appl	647	21	21.2	10	5	PCT-US94-02631-27	Sequence 27, Appl
575	22	22.2	23	1	US-08-248-819A-23	Sequence 23, Appl	648	21	21.2	10	5	PCT-US94-02631-66	Sequence 66, Appl
576	22	22.2	23	2	US-08-337-646A-41	Sequence 41, Appl	650	21	21.2	10	5	PCT-US95-03236-6	Sequence 6, Appl
577	22	22.2	23	2	US-08-856-531-21	Sequence 21, Appl	651	21	21.2	11	1	US-08-217-188A-51	Sequence 51, Appl
578	22	22.2	23	4	US-08-856-034-21	Sequence 21, Appl	652	21	21.2	11	1	US-08-469-582-10	Sequence 10, Appl
579	22	22.2	23	4	US-09-029-348-8	Sequence 8, Appl	653	21	21.2	11	1	US-08-687-226-51	Sequence 51, Appl
580	22	22.2	23	4	US-08-927-326-41	Sequence 41, Appl	654	21	21.2	11	1	US-08-476-405A-27	Sequence 27, Appl
581	22	22.2	23	4	US-09-585-887-2	Sequence 2, Appl	655	21	21.2	11	1	US-08-218-026-43	Sequence 43, Appl
582	22	22.2	23	4	US-09-289-578-2	Sequence 2, Appl	656	21	21.2	11	1	US-08-342-930-4	Sequence 4, Appl
583	22	22.2	23	4	US-09-125-138-4	Sequence 4, Appl	657	21	21.2	11	2	US-08-653-632-43	Sequence 43, Appl
584	22	22.2	24	2	US-08-306-078-6	Sequence 6, Appl	658	21	21.2	11	2	US-08-669-721-19	Sequence 19, Appl
585	22	22.2	24	2	US-09-047-026A-12	Sequence 12, Appl	659	21	21.2	11	2	US-08-473-025-7	Sequence 7, Appl
586	22	22.2	24	3	US-08-504-558A-8	Sequence 8, Appl	660	21	21.2	11	3	US-08-667-725B-51	Sequence 51, Appl
587	22	22.2	24	4	US-09-249-458A-8	Sequence 8, Appl	661	21	21.2	11	4	US-09-007-748-51	Sequence 51, Appl
588	22	22.2	24	4	US-09-230-548-27	Sequence 27, Appl	662	21	21.2	11	4	US-09-189-344-19	Sequence 19, Appl
589	22	22.2	24	4	US-09-227-357-524	Sequence 524, App	663	21	21.2	11	4	US-09-206-059-17	Sequence 17, Appl
590	22	22.2	24	4	US-09-043-731-20	Sequence 20, Appl	664	21	21.2	11	4	US-09-027-108C-4	Sequence 4, Appl
591	22	22.2	24	4	US-08-630-052-8	Sequence 8, Appl	665	21	21.2	12	1	US-08-260-582-55	Sequence 55, Appl
592	22	22.2	24	5	PCT-US95-09307-8	Sequence 8, Appl	666	21	21.2	12	1	US-08-469-582-20	Sequence 20, Appl
593	22	22.2	25	1	US-07-754-918A-3	Sequence 3, Appl	667	21	21.2	12	1	US-08-469-582-21	Sequence 21, Appl
594	22	22.2	25	1	US-08-248-839C-184	Sequence 184, App	668	21	21.2	12	1	US-08-671-525B-15	Sequence 15, Appl
595	22	22.2	25	4	US-09-025-596-38	Sequence 38, Appl	669	21	21.2	12	1	US-08-671-525B-20	Sequence 20, Appl
596	21.5	21.7	23	4	US-08-395-602A-3	Sequence 3, Appl	670	21	21.2	12	1	US-08-671-525B-22	Sequence 22, Appl
597	21.5	21.7	23	2	US-08-021-625D-3	Sequence 3, Appl	671	21	21.2	12	1	US-08-671-525B-23	Sequence 23, Appl
598	21.5	21.7	24	5	US-09-392-277-28	Sequence 28, Appl	672	21	21.2	12	1	US-08-671-525B-23	Sequence 23, Appl
599	21	21.2	24	3	US-08-941-532-3	Sequence 3, Appl	673	21	21.2	12	1	US-08-672-109B-15	Sequence 15, Appl
600	21	21.2	24	3	US-09-006-428A-22	Sequence 22, Appl	674	21	21.2	12	1	US-08-672-109B-20	Sequence 20, Appl
601	21	21.2	24	5	US-07-634-634B-1	Sequence 1, Appl	675	21	21.2	12	1	US-08-672-109B-21	Sequence 21, Appl
602	21	21.2	24	6	US-08-482-228-145	Sequence 145, App	676	21	21.2	12	1	US-08-672-109B-22	Sequence 22, Appl
603	21	21.2	24	6	US-08-482-528-145	Sequence 145, App	677	21	21.2	12	1	US-08-672-109B-23	Sequence 23, Appl
604	21	21.2	24	6	US-08-941-532-2	Sequence 2, Appl	678	21	21.2	12	1	US-08-548-540-155	Sequence 155, App
605	21	21.2	24	6	US-08-513-966-61	Sequence 61, Appl	679	21	21.2	12	1	US-08-191-338A-12	Sequence 12, Appl
606	21	21.2	24	6	US-09-020-880-55	Sequence 55, Appl	680	21	21.2	12	2	US-08-842-045-15	Sequence 15, Appl
607	21	21.2	24	6	US-08-635-928-13	Sequence 13, Appl	681	21	21.2	12	2	US-08-842-045-20	Sequence 20, Appl
608	21	21.2	24	6	US-09-101-544-55	Sequence 55, Appl	682	21	21.2	12	2	US-08-842-045-21	Sequence 21, Appl
609	21	21.2	24	7	US-09-006-428A-21	Sequence 21, Appl	683	21	21.2	12	2	US-08-842-045-22	Sequence 22, Appl
610	21	21.2	24	7	US-08-545-228-1	Sequence 1, Appl	684	21	21.2	12	2	US-08-842-045-23	Sequence 23, Appl
611	21	21.2	24	7	US-08-776-585-12	Sequence 12, Appl							

685	21	21.2	12	2	US-08-842-238-15	Sequence 15, Appl	758	21	21.2	15	2	US-07-847-311A-8	Sequence 8, Appl
686	21	21.2	12	2	US-08-842-238-20	Sequence 20, Appl	759	21	21.2	15	2	US-08-986-234-23	Sequence 23, Appl
687	21	21.2	12	2	US-08-842-238-21	Sequence 21, Appl	760	21	21.2	15	4	US-08-930-917A-9	Sequence 9, Appl
688	21	21.2	12	2	US-08-842-238-22	Sequence 22, Appl	761	21	21.2	15	4	US-08-604-365-30	Sequence 30, Appl
689	21	21.2	12	2	US-08-842-238-23	Sequence 23, Appl	762	21	21.2	15	4	US-09-035-098-3	Sequence 3, Appl
690	21	21.2	12	2	US-08-637-759B-407	Sequence 407, App	763	21	21.2	15	4	US-08-060-988A-42	Sequence 42, Appl
691	21	21.2	12	2	US-08-538-711A-2	Sequence 2, Appl1	764	21	21.2	15	5	PCT-US93-06751-25	Sequence 25, Appl
692	21	21.2	12	2	US-08-871-355A-407	Sequence 407, App	765	21	21.2	15	5	PCT-US93-06751-48	Sequence 48, Appl
693	21	21.2	12	3	US-08-629-335B-15	Sequence 15, Appl	766	21	21.2	15	5	PCT-US93-06751-75	Sequence 75, Appl
694	21	21.2	12	3	US-08-629-335B-20	Sequence 20, Appl	767	21	21.2	15	5	PCT-US93-06751-107	Sequence 107, App
695	21	21.2	12	3	US-08-629-335B-21	Sequence 21, Appl	768	21	21.2	16	1	PCT-US95-04018-23	Sequence 23, Appl
696	21	21.2	12	3	US-08-629-335B-22	Sequence 22, Appl	769	21	21.2	16	1	US-08-053-616-4	Sequence 4, Appl
697	21	21.2	12	3	US-08-629-335B-23	Sequence 23, Appl	770	21	21.2	16	1	US-07-994-469A-21	Sequence 21, Appl
698	21	21.2	12	4	US-09-258-754-88	Sequence 88, Appl	771	21	21.2	16	1	US-07-994-657-3	Sequence 3, Appl
699	21	21.2	12	4	US-09-042-107-88	Sequence 88, Appl	772	21	21.2	16	1	US-07-942-245-95	Sequence 95, Appl
700	21	21.2	12	4	US-08-725-027-2	Sequence 2, Appl1	773	21	21.2	16	1	US-07-942-245-96	Sequence 96, Appl
701	21	21.2	12	4	US-09-201-945-407	Sequence 407, App	774	21	21.2	16	1	US-07-942-245-97	Sequence 97, Appl
702	21	21.2	12	4	US-09-027-108C-5	Sequence 5, Appl1	775	21	21.2	16	1	US-07-942-245-102	Sequence 102, App
703	21	21.2	12	4	US-09-638-302A-118	Sequence 118, App	776	21	21.2	16	1	US-07-942-245-118	Sequence 118, App
704	21	21.2	12	5	PCT-US95-05471-55	Sequence 55, Appl	777	21	21.2	16	1	US-07-942-245-122	Sequence 122, App
705	21	21.2	12	5	PCT-US96-09809-155	Sequence 155, App	778	21	21.2	16	1	US-07-942-245-146	Sequence 146, App
706	21	21.2	12	6	5210075-52	Patent No. 5210075	779	21	21.2	16	1	US-07-942-245-175	Sequence 175, App
707	21	21.2	13	1	US-08-469-582-2	Sequence 2, Appl1	780	21	21.2	16	1	US-08-077-787A-1	Sequence 1, Appl1
708	21	21.2	13	1	US-08-469-582-18	Sequence 18, Appl	781	21	21.2	16	1	US-08-474-567-3	Sequence 3, Appl1
709	21	21.2	13	4	US-08-946-525-8	Sequence 8, Appl1	782	21	21.2	16	2	US-08-337-646A-16	Sequence 16, Appl
710	21	21.2	13	4	US-08-392-542-5	Sequence 5, Appl1	783	21	21.2	16	2	US-08-368-834-8	Sequence 8, Appl
711	21	21.2	13	4	US-09-206-059-12	Sequence 12, Appl	784	21	21.2	16	2	US-08-447-154-8	Sequence 8, Appl
712	21	21.2	13	4	US-09-177-249-34	Sequence 34, Appl	785	21	21.2	16	3	US-08-556-965-25	Sequence 25, Appl
713	21	21.2	13	4	US-08-894-327-5	Sequence 5, Appl1	786	21	21.2	16	3	US-08-556-965-19	Sequence 19, Appl
714	21	21.2	13	4	US-09-261-855-6	Sequence 6, Appl1	787	21	21.2	16	3	US-08-604-965E-5	Sequence 5, Appl1
715	21	21.2	13	4	US-08-687-590-68	Sequence 68, Appl	788	21	21.2	16	3	US-08-736-915-5	Sequence 5, Appl1
716	21	21.2	13	4	US-09-685-027-5	Sequence 5, Appl1	789	21	21.2	16	4	US-08-927-326-16	Sequence 16, Appl
717	21	21.2	13	4	US-09-599-286-8	Sequence 8, Appl1	790	21	21.2	16	4	US-08-602-999A-169	Sequence 169, App
718	21	21.2	13	5	PCT-US94-10257A-50	Sequence 50, Appl	791	21	21.2	16	4	US-09-500-124-169	Sequence 1, Appl1
719	21	21.2	14	1	US-08-164-618-12	Sequence 12, Appl	792	21	21.2	16	5	5278286-4	Sequence 1, Appl1
720	21	21.2	14	1	US-08-164-618-13	Sequence 13, Appl	793	21	21.2	17	1	US-08-066-239-7	Sequence 7, Appl1
721	21	21.2	14	1	US-08-164-618-14	Sequence 14, Appl	794	21	21.2	17	1	US-08-265-047-11	Sequence 11, Appl
722	21	21.2	14	1	US-08-164-618-15	Sequence 15, Appl	795	21	21.2	17	2	US-08-424-268-4	Sequence 4, Appl1
723	21	21.2	14	1	US-08-164-618-19	Sequence 19, Appl	796	21	21.2	17	2	US-08-824-151-1	Sequence 1, Appl1
724	21	21.2	14	1	US-07-694-469A-20	Sequence 20, Appl	797	21	21.2	17	2	US-08-824-151-2	Sequence 2, Appl1
725	21	21.2	14	1	US-08-111-080-6	Sequence 6, Appl1	798	21	21.2	17	2	US-08-621-803-6	Sequence 6, Appl1
726	21	21.2	14	1	US-08-258-851-7	Sequence 7, Appl1	799	21	21.2	17	2	US-08-429-964-68	Sequence 68, Appl
727	21	21.2	14	1	US-08-211-980-6	Sequence 6, Appl1	800	21	21.2	17	2	US-09-115-209-8	Sequence 8, Appl
728	21	21.2	14	1	US-08-321-668-21	Sequence 21, Appl	801	21	21.2	17	2	US-09-217-352-6	Sequence 6, Appl1
729	21	21.2	14	1	US-08-321-668-25	Sequence 25, Appl	802	21	21.2	17	4	US-08-918-428D-15	Sequence 15, Appl
730	21	21.2	14	1	US-08-321-668-40	Sequence 40, Appl	803	21	21.2	17	4	PCT-US93-08062-68	Sequence 20, Appl
731	21	21.2	14	1	US-08-321-668-41	Sequence 41, Appl	804	21	21.2	17	5	PCT-US93-10442-4	Sequence 4, Appl1
732	21	21.2	14	1	US-08-321-668-42	Sequence 42, Appl	805	21	21.2	17	5	5219837-8	Sequence 8, Appl1
733	21	21.2	14	1	US-08-837-941-21	Sequence 21, Appl	806	21	21.2	17	6	US-08-325-243A-15	Sequence 15, Appl
734	21	21.2	14	1	US-08-837-941-25	Sequence 25, Appl	807	21	21.2	18	1	US-07-876-941A-29	Sequence 29, Appl
735	21	21.2	14	1	US-08-837-941-40	Sequence 40, Appl	808	21	21.2	18	2	US-08-649-991-48	Sequence 48, Appl
736	21	21.2	14	1	US-08-837-941-41	Sequence 41, Appl	809	21	21.2	18	2	US-08-649-991-55	Sequence 55, Appl
737	21	21.2	14	1	US-08-837-941-42	Sequence 42, Appl	810	21	21.2	18	2	US-09-017-205-61	Sequence 61, Appl
738	21	21.2	14	1	US-08-476-405A-24	Sequence 24, Appl	811	21	21.2	18	2	US-08-476-866-8	Sequence 8, Appl1
739	21	21.2	14	4	US-08-448-489-8	Sequence 8, Appl1	812	21	21.2	18	2	US-08-604-365-31	Sequence 31, Appl
740	21	21.2	14	4	US-08-895-590-22	Sequence 22, Appl	813	21	21.2	18	2	US-08-476-866-8	Sequence 8, Appl1
741	21	21.2	14	4	US-08-895-590-22	Sequence 22, Appl	814	21	21.2	18	2	US-08-604-365-31	Sequence 31, Appl
742	21	21.2	14	4	US-08-687-590-40	Sequence 40, Appl	815	21	21.2	18	4	US-08-895-590-28	Sequence 28, Appl
743	21	21.2	14	5	PCT-US81-08328-36	Sequence 36, Appl	816	21	21.2	18	4	US-09-142-680-23	Sequence 23, Appl
744	21	21.2	14	5	PCT-US92-07111-6	Sequence 6, Appl1	817	21	21.2	18	4	5187077-36	Sequence 8, Appl1
745	21	21.2	14	5	PCT-US93-07967-6	Sequence 90, Appl	818	21	21.2	18	5	5427925-34	Sequence 34, Appl
746	21	21.2	14	5	US-07-859-291C-5	Sequence 5, Appl1	819	21	21.2	18	6	US-08-634-060-42	Sequence 42, Appl
747	21	21.2	15	1	US-08-221-583-23	Sequence 23, Appl	820	21	21.2	19	1	US-08-448-194-37	Sequence 37, Appl
748	21	21.2	15	1	US-08-218-025A-185	Sequence 185, App	821	21	21.2	19	3	US-08-667-921-37	Sequence 92, Appl
749	21	21.2	15	1	US-08-208-181A-18	Sequence 18, Appl	822	21	21.2	19	4	US-08-399-646-9	Sequence 9, Appl1
750	21	21.2	15	1	US-08-095-332-8	Sequence 8, Appl1	823	21	21.2	19	4	US-08-111-080-9	Sequence 9, Appl1
751	21	21.2	15	1	US-08-625-691-2	Sequence 2, Appl1	824	21	21.2	20	1	US-07-951-715A-75	Sequence 75, Appl
752	21	21.2	15	1	US-07-760-530-8	Sequence 8, Appl1	825	21	21.2	20	1	US-08-208-181A-3	Sequence 3, Appl1
753	21	21.2	15	2	US-08-454-267-3	Sequence 3, Appl1	826	21	21.2	20	1	US-08-211-980-9	Sequence 9, Appl1
754	21	21.2	15	2	US-08-583-569-2	Sequence 2, Appl1	827	21	21.2	20	1		
755	21	21.2	15	2	US-08-583-569-2	Sequence 2, Appl1	828	21	21.2	20	1		
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757	21	21.2	15	2	US-08-583-569-2	Sequence 2, Appl1	830	21	21.2	20	1		

831	21	21.2	20	1	US-08-607-321-9	Sequence 9, App11	904	21	21.2	23	3	US-08-646-273-1	Sequence 1, App11
832	21	21.2	20	2	US-08-961-240-9	Sequence 9, App11	905	21	21.2	23	4	US-08-736-915-7	Sequence 12, App1
833	21	21.2	20	2	US-08-605-501-9	Sequence 27, App1	906	21	21.2	23	4	US-09-150-660B-12	Sequence 6, App1
834	21	21.2	20	2	US-08-337-646A-27	Sequence 27, App1	907	21	21.2	23	4	US-08-734-607B-16	Sequence 14, App1
835	21	21.2	20	2	US-08-459-448A-75	Sequence 75, App1	908	21	21.2	23	4	US-09-230-548-14	Sequence 11, App1
836	21	21.2	20	2	US-08-591B-24	Sequence 24, App1	909	21	21.2	23	4	US-09-028-937-11	Sequence 10, App1
837	21	21.2	20	3	US-08-459-595A-75	Sequence 75, App1	910	21	21.2	23	5	PCT-US92-07111-10	Sequence 10, App1
838	21	21.2	20	3	US-08-872-094-13	Sequence 13, App1	911	21	21.2	23	5	PCT-US93-07967-12	Sequence 10, App1
839	21	21.2	20	3	US-08-459-504B-75	Sequence 75, App1	912	21	21.2	24	2	US-08-146-028-72	Sequence 10, App1
840	21	21.2	20	3	US-08-513-968-64	Sequence 64, App1	913	21	21.2	24	3	US-08-467-923-193	Sequence 193, App
841	21	21.2	20	3	US-08-459-444-75	Sequence 75, App1	914	21	21.2	24	4	US-08-855-958-6	Sequence 6, App1
842	21	21.2	20	4	US-08-612-973-66	Sequence 66, App1	915	21	21.2	24	4	US-08-723-425A-72	Sequence 72, App1
843	21	21.2	20	4	US-08-392-542-8	Sequence 8, App11	916	21	21.2	24	4	US-08-392-542-10	Sequence 10, App1
844	21	21.2	20	4	US-08-392-542-9	Sequence 9, App11	917	21	21.2	24	4	US-09-112-006-12	Sequence 12, App1
845	21	21.2	20	4	US-08-505-250-23	Sequence 23, App1	918	21	21.2	24	4	US-09-098-901-6	Sequence 6, App11
846	21	21.2	20	4	US-08-927-326-27	Sequence 27, App1	919	21	21.2	24	4	US-08-894-327-10	Sequence 10, App1
847	21	21.2	20	4	US-08-927-326-27	Sequence 27, App1	920	21	21.2	24	4	US-09-230-548-18	Sequence 18, App1
848	21	21.2	20	4	US-08-894-327-6	Sequence 66, App1	921	21	21.2	24	4	US-09-230-548-19	Sequence 18, App1
849	21	21.2	20	4	US-08-894-327-9	Sequence 8, App11	922	21	21.2	24	4	US-09-230-548-30	Sequence 29, App1
850	21	21.2	20	4	US-08-341-555-1	Sequence 9, App11	923	21	21.2	25	4	US-09-685-027-10	Sequence 30, App1
851	21	21.2	20	4	US-09-330-740A-1	Sequence 1, App11	924	21	21.2	25	1	US-07-976-358-10	Sequence 20, App1
852	21	21.2	20	4	US-09-547-422-75	Sequence 75, App1	925	21	21.2	25	1	US-08-209-525-32	Sequence 32, App1
853	21	21.2	20	4	US-08-505-250-23	Sequence 23, App1	926	21	21.2	25	1	US-08-362-567-2	Sequence 2, App11
854	21	21.2	20	4	US-09-304-711-24	Sequence 24, App1	927	21	21.2	25	2	US-08-677-298-3	Sequence 3, App11
855	21	21.2	20	4	US-09-685-027-8	Sequence 8, App11	928	21	21.2	25	3	US-08-846-444-7	Sequence 7, App11
856	21	21.2	20	4	US-09-685-027-9	Sequence 9, App11	929	21	21.2	25	4	US-08-392-542-11	Sequence 11, App1
857	21	21.2	20	4	US-09-643-597-242	Sequence 242, App	930	21	21.2	25	4	US-08-894-327-11	Sequence 11, App1
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859	21	21.2	20	4	US-09-643-597-246	Sequence 246, App	932	21	21.2	25	4	US-09-227-357-334	Sequence 334, App
860	21	21.2	20	4	US-09-643-597-367	Sequence 367, App	933	21	21.2	25	4	US-09-685-027-11	Sequence 11, App1
861	21	21.2	20	4	US-09-173-281-24	Sequence 24, App1	934	21	21.2	25	6	5178861-14	Patent No. 5178861
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863	21	21.2	20	5	PCT-US94-07967-9	Sequence 9, App11	936	20.5	20.7	15	2	US-08-811-028-12	Sequence 52, App1
864	21	21.2	20	5	PCT-US94-10257A-78	Sequence 78, App1	937	20.5	20.7	15	2	PCT-US92-10068-16	Sequence 16, App1
865	21	21.2	21	1	US-08-119-169A-1	Sequence 79, App1	938	20.5	20.7	15	6	5187155-21	Patent No. 5187155
866	21	21.2	21	1	US-08-279-906A-20	Sequence 20, App11	939	20.5	20.7	17	2	US-09-115-209-47	Sequence 47, App1
867	21	21.2	21	1	US-08-053-131-85	Sequence 85, App1	940	20.5	20.7	17	2	US-09-115-209-48	Sequence 48, App1
868	21	21.2	21	1	US-08-645-641-85	Sequence 85, App1	941	20.5	20.7	18	4	US-08-535-661-17	Sequence 17, App1
869	21	21.2	21	1	US-08-476-405A-13	Sequence 13, App1	942	20.5	20.7	19	4	US-08-535-661-18	Sequence 18, App1
870	21	21.2	21	1	US-07-853-408B-85	Sequence 85, App1	943	20.5	20.7	20	1	US-07-718-274A-7	Sequence 7, App11
871	21	21.2	21	1	US-08-096-762-85	Sequence 85, App1	944	20.5	20.7	20	1	US-07-718-274A-12	Sequence 12, App1
872	21	21.2	21	2	US-08-308-865-85	Sequence 85, App1	945	20.5	20.7	20	1	US-07-718-274A-29	Sequence 29, App1
873	21	21.2	21	2	US-08-675-631-2	Sequence 2, App11	946	20.5	20.7	20	1	US-08-149-106-7	Sequence 7, App11
874	21	21.2	21	2	US-08-675-631-10	Sequence 10, App1	947	20.5	20.7	20	1	US-08-149-106-12	Sequence 12, App1
875	21	21.2	21	4	US-08-957-001B-23	Sequence 23, App1	948	20.5	20.7	20	1	US-08-149-106-29	Sequence 29, App1
876	21	21.2	21	4	US-09-486-301-23	Sequence 23, App1	949	20.5	20.7	20	1	US-08-298-021-7	Sequence 7, App11
877	21	21.2	21	4	US-09-042-353-282	Sequence 282, App	950	20.5	20.7	20	1	US-08-298-021-12	Sequence 12, App1
878	21	21.2	21	4	US-08-756-417A-130	Sequence 130, App	951	20.5	20.7	20	1	US-08-298-021-29	Sequence 29, App1
879	21	21.2	21	4	US-09-286-959B-21	Sequence 21, App1	952	20.5	20.7	20	4	US-08-535-661-19	Sequence 19, App1
880	21	21.2	21	4	US-09-508-803-3	Sequence 3, App11	953	20.5	20.7	20	4	US-09-064-411A-48	Sequence 48, App1
881	21	21.2	21	4	PCT-US92-10983-85	Sequence 85, App1	954	20.5	20.7	21	4	US-08-535-661-20	Sequence 20, App1
882	21	21.2	21	5	US-07-933-469A-7	Sequence 7, App11	955	20.5	20.7	22	1	US-07-696-928A-1	Sequence 1, App11
883	21	21.2	22	1	US-08-250-310-7	Sequence 7, App11	956	20.5	20.7	22	1	US-08-535-661-21	Sequence 21, App1
884	21	21.2	22	1	US-08-439-404-7	Sequence 7, App11	957	20.5	20.7	22	4	US-07-696-928A-8	Sequence 8, App11
885	21	21.2	22	1	US-08-321-658-6	Sequence 6, App11	958	20.5	20.7	24	1	US-08-782-997A-35	Sequence 35, App1
886	21	21.2	22	1	US-08-837-941-6	Sequence 6, App11	959	20.5	20.7	24	4	US-08-535-661-23	Sequence 23, App1
887	21	21.2	22	1	US-08-484-635-134	Sequence 134, App	960	20.5	20.7	25	4	US-08-406-132-42	Sequence 42, App1
888	21	21.2	22	1	US-08-143-311B-1	Sequence 1, App11	961	20.5	20.7	25	1	US-08-169-743-2	Sequence 2, App11
889	21	21.2	22	1	US-08-345-321-19	Sequence 19, App1	962	20.5	20.7	25	1	US-08-178-482-7	Sequence 7, App11
890	21	21.2	22	2	US-08-827-570-134	Sequence 134, App	963	20.5	20.7	25	1	US-08-234-997-1	Sequence 1, App11
891	21	21.2	22	2	US-09-340-781B-7	Sequence 7, App11	964	20.5	20.7	26	1	US-08-733-505A-5	Sequence 5, App11
892	21	21.2	22	3	US-08-753-851-1	Sequence 1, App11	965	20.5	20.7	26	1	US-08-345-321-13	Sequence 13, App1
893	21	21.2	22	3	PCT-US92-08094-5	Sequence 10, App1	966	20.5	20.7	26	2	US-08-747-137-74	Sequence 74, App1
894	21	21.2	22	3	US-08-111-080-10	Sequence 10, App1	967	20.5	20.7	26	2	US-08-747-137-176	Sequence 176, App
895	21	21.2	22	3	US-08-211-980-10	Sequence 10, App1	968	20.5	20.7	26	3	US-09-020-880-52	Sequence 52, App1
896	21	21.2	22	3	US-08-487-001A-29	Sequence 29, App1	969	20.5	20.7	26	3	US-09-020-880-60	Sequence 60, App1
897	21	21.2	22	3	US-08-630-832A-29	Sequence 29, App1	970	20.5	20.7	26	4	US-09-178-115-103	Sequence 103, App
898	21	21.2	22	3	US-09-005-069-29	Sequence 29, App1	971	20.5	20.7	26	4		
899	21	21.2	22	3			972	20.5	20.7	26	4		
900	21	21.2	22	3			973	20.5	20.7	26	4		
901	21	21.2	22	3			974	20.5	20.7	26	4		
902	21	21.2	22	3			975	20.5	20.7	26	4		
903	21	21.2	22	3			976	20.5	20.7	26	4		

977 20 20.2 6 4 US-09-101-544-52 Sequence 52, Appl
978 20 20.2 6 4 US-09-101-544-60 Sequence 60, Appl
979 20 20.2 6 4 US-09-606-477-1 Sequence 1, Appl
980 20 20.2 6 5 PCT-US93-05640-45 Sequence 45, Appl
981 20 20.2 7 1 US-08-421-702A-12 Sequence 12, Appl
982 20 20.2 7 1 US-08-303-052A-12 Sequence 12, Appl
983 20 20.2 7 1 US-08-421-696A-12 Sequence 12, Appl
984 20 20.2 7 1 US-08-421-697A-12 Sequence 12, Appl
985 20 20.2 7 1 US-08-421-698A-12 Sequence 12, Appl
986 20 20.2 7 2 US-08-421-695A-12 Sequence 12, Appl
987 20 20.2 7 5 PCT-US95-04741-12 Sequence 12, Appl
988 20 20.2 8 1 US-08-468-674B-83 Sequence 83, Appl
989 20 20.2 8 1 US-08-403-634-13 Sequence 13, Appl
990 20 20.2 8 1 US-08-403-634-13 Sequence 13, Appl
991 20 20.2 8 1 US-08-780-571-83 Sequence 83, Appl
992 20 20.2 8 1 US-08-747-137-75 Sequence 75, Appl
993 20 20.2 8 3 US-08-785-247-26 Sequence 26, Appl
994 20 20.2 8 4 US-08-913-441B-9 Sequence 9, Appl
995 20 20.2 8 4 US-08-913-441B-13 Sequence 13, Appl
996 20 20.2 8 4 US-09-108-857-7 Sequence 7, Appl
997 20 20.2 9 1 US-08-445-745-114 Sequence 114, App
998 20 20.2 9 2 US-08-101-624-17 Sequence 17, Appl
999 20 20.2 9 2 US-08-986-234-40 Sequence 40, Appl
1000 20 20.2 9 3 US-08-159-339A-334 Sequence 334, App

ALIGNMENTS

RESULT 1
US-08-726-306A-61
Sequence 61, Application US/08726306A

Patent No. 5958684

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem

APPLICANT: Burbach, Johannes Peter Henri

APPLICANT: Grosveld, Franklin G.

TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS

NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1 Financial Center

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,306A

FILING DATE: 02-Oct-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 95/20080.4

FILING DATE: 02-Oct-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/009,832

FILING DATE: 01-Jan-1996

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Ph.D., Kathleen M.

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100

TELEFAX: (617) 345-9111

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-726-306A-61

Query Match 100.0%; Score 99; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NVPGHERMGRGRTSSKELA 19

Db 7 NVPGHERMGRGRTSSKELA 25

RESULT 2
US-08-726-306A-87

Sequence 87, Application US/08726306A

Patent No. 5958684

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem

APPLICANT: Burbach, Johannes Peter Henri

APPLICANT: Grosveld, Franklin G.

TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS

NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1 Financial Center

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,306A

FILING DATE: 02-Oct-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 95/20080.4

FILING DATE: 02-Oct-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/009,832

FILING DATE: 01-Jan-1996

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Ph.D., Kathleen M.

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100

TELEFAX: (617) 345-9111

INFORMATION FOR SEQ ID NO: 87:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-726-306A-87

Query Match 100.0%; Score 99; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NVPGHERMGRGRTSSKELA 19

Db 7 NVPGHERMGRGRTSSKELA 25

RESULT 3
US-08-726-306A-1

Sequence 1, Application US/08726306A

Patent No. 5958684

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-1

Query Match 47.5%; Score 47; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RGRSSKELA 19
|||
Db 1 RGRSSKELA 10

RESULT 4
US-09-540-224-9
Sequence 9, Application US/09540224
Patent No. 6468543
GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 24
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide

US-09-540-224-9

Query Match 33.8%; Score 33.5; DB 4; Length 24;
Best Local Similarity 58.3%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 3 PGHERMGRGRTSS 13
|||
Db 4 PGHRRGRRAKT 15

RESULT 5
US-08-077-797A-34
Sequence 34, Application US/08077797A
Patent No. 5679548
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Rosenblum, Jonathan
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL
TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5679548th Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,797A
FILING DATE: 14-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1276P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-077-797A-34

Query Match 32.3%; Score 32; DB 1; Length 16;
Best Local Similarity 38.5%; Pred. No. 21;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGHERMGRGRTSS 15
|||
Db 4 PGHRRGRRAKSDS 16

RESULT 6
PCT-US94-01238-34
Sequence 34, Application PC/TUS9401238
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL

```
; TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
; NUMBER OF SEQUENCES: 65
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01238
; FILING DATE: 01-FEB-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,797
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,566
; FILING DATE: 02-FEB-1993
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; PCT-US94-01238-34

Query Match          32.3%; Score 32; DB 5; Length 16;
Best Local Similarity 38.5%; Pred. No. 21;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PGHERMGGRGRTSS 15
Db      4 PGRRRLGQALSDS 16

RESULT 7
US-07-841-591A-11
; Sequence 11, Application US/07841591A
; Patent No. 5900476
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M. and
; APPLICANT: Ware, Jerry, inventors
; APPLICANT: on behalf of The Scripps Research
; TITLE OF INVENTION: Therapeutic Domains of
; TITLE OF INVENTION: von Willebrand Factor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 No. 5900476th Torrey Pines Road
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.2 megabyte 5 1/4" floppy
; COMPUTER: AST Bravo 386SX
; OPERATING SYSTEM: MS DOS version 3.2
; SOFTWARE: Wordperfect 5.1 conv. to ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,591A
; FILING DATE: 26-FEB-92
; CLASSIFICATION:
; PRIOR APPLICATION DATA: This is a c-i-p of
; APPLICATION NUMBER: PCT/US91/07756
; FILING DATE: 17-Oct-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Barron, Alexis
; REGISTRATION NUMBER: 22,702
; REFERENCE/DOCKET NUMBER: P16,633-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 923-4466
; TELEFAX: (215) 923-2189
; INFORMATION FOR SEQ ID NO: 11:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-07-841-591A-11

Query Match          32.3%; Score 32; DB 2; Length 21;
Best Local Similarity 35.3%; Pred. No. 28;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      1 NVPGHERMGGRGRTSSKE 17
Db      3 SMTGGQGMGRGSPGLQE 19

RESULT 8
PCT-US93-02034-11
; Sequence 11, Application PC/TUS9302034
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M. and
; APPLICANT: Ware, Jerry, inventors
; APPLICANT: on behalf of The Scripps Research
; APPLICANT: Institute
; TITLE OF INVENTION: Therapeutic Domains of
; TITLE OF INVENTION: von Willebrand Factor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 North Torrey Pines Road
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 2 megabyte 3.25" floppy
; COMPUTER: AST Bravo 386SX
; OPERATING SYSTEM: MS DOS version 3.2
; SOFTWARE: Wordperfect 5.1 conv. to ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02034
; FILING DATE: 19930223
; CLASSIFICATION:
; PRIOR APPLICATION DATA: This is a c-i-p of
; APPLICATION NUMBER: PCT/US91/07756
; FILING DATE: 17-Oct-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Barron, Alexis
; REGISTRATION NUMBER: 22,702
; REFERENCE/DOCKET NUMBER: P16,633-H PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 923-4466
; TELEFAX: (215) 923-2189
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
; PCT-US93-02034-11

Query Match          32.3%; Score 32; DB 5; Length 21;
Best Local Similarity 35.3%; Pred. No. 28;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      1 NVPGHERMGGRGRTSSKE 17
Db      3 SMTGGQGMGRGSPGLQE 19

RESULT 9
US-09-047-026A-9
; Sequence 9, Application US/09047026A
```



```

1 OPERATING SYSTEM: PC-DOS/MS-DOS
2 SOFTWARE: PatentIn Release #1.0, Version #1.25
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: PCT/US93/06751
5 FILING DATE: 19930719
6 CLASSIFICATION:
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Meredith, Roy D.
9 REGISTRATION NUMBER: 30,777
10 REFERENCE/DOCKET NUMBER: 18614
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: (908) 594-4678
13 TELEFAX: (908) 594-4720
14 TELEX: 138825
15 INFORMATION FOR SEQ ID NO: 106:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 14 amino acids
18 TYPE: amino acid
19 STRANDEDNESS: single
20 TOPOLOGY: linear
21 MOLECULE TYPE: peptide
22 HYPOTHEetical: NO
23 ANTI-SENSE: NO
24 IMMEDIATE SOURCE: Random Epitope Library Delta
25 PCT-US93-06751-106
26
27 Query Match 31.3%; Score 31; DB 5; Length 14;
28 Best Local Similarity 46.2%; Pred. No. 26;
29 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
30
31 OY 4 GHERMGRGRTSSK 16
32 |:::| |||::|
33 Db 1 GVVKLGPERTAGK 13
34
35 RESULT 11
36 US-07-942-245-142
37 Sequence 142, Application US/07942245
38 Patent No. 5639641
39 GENERAL INFORMATION:
40 APPLICANT: PEDERSEN, Jan T.
41 APPLICANT: SEARLE, Stephen M. J.
42 APPLICANT: REES, Anthony R.
43 APPLICANT: ROGUSKA, Michael A.
44 APPLICANT: GUILD, Braydon C.
45 TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
46 TITLE OF INVENTION: ANTIBODIES
47 NUMBER OF SEQUENCES: 522
48 CORRESPONDENCE ADDRESS:
49 ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
50 STREET: 2100 Pennsylvania Avenue, N.W.
51 CITY: Washington
52 STATE: D.C.
53 COUNTRY: United States
54 ZIP: 20037-3202
55 COMPUTER READABLE FORM:
56 MEDIUM TYPE: floppy disk
57 COMPUTER: HP 9000/700 Workstation
58 OPERATING SYSTEM: UNIX
59 SOFTWARE: In house
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: US/07/942,245
62 FILING DATE: 09-SEP-1992
63 CLASSIFICATION: 530
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: (202) 293-7060
66 TELEFAX: (202) 293-7860
67 TELEX: 6491103
68 INFORMATION FOR SEQ ID NO: 142:
69 SEQUENCE CHARACTERISTICS:
70 LENGTH: 16 amino acids
71 TYPE: amino acid
72 TOPOLOGY: linear

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MOLECULE TYPE: peptide
US-07-942-245-142

Query Match 31.3%; Score 31; DB 1; Length 16;
Best Local Similarity 58.3%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 RMGRGRTSSKEL 18
| | | | | | | | | | | | | | | | | |
DB 5 RPRGRSSSEKL 16

RESULT 12

US-09-166-028-3
Sequence 3, Application US/09166028
Patent No. 6245885
GENERAL INFORMATION:
APPLICANT: Gordon C. Shore et al.
TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
FILE REFERENCE: 50013/011001
CURRENT APPLICATION NUMBER: US/09/166,028
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-028-3

Query Match 31.3%; Score 31; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 4 GHERMGRGRTSSKEL 18
| | | | | | | | | | | | | | | | | |
DB 5 GEGPRGGGPTSSSEQI 19

RESULT 13
US-08-874-569B-14
Sequence 14, Application US/08874569B
Patent No. 6306650
GENERAL INFORMATION:
APPLICANT: Townes, Tim M.
TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
FILE REFERENCE: 05118.000802
CURRENT APPLICATION NUMBER: US/08/874,569B
CURRENT FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/019,769
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: \ No. 6306650e =
US-08-874-569B-14

Query Match 31.3%; Score 31; DB 4; Length 23;
Best Local Similarity 40.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 4 GHERMGRGRTSSKEL 18
| | | | | | | | | | | | | | | | | |
DB 2 GHGGCGKSKSSSHL 16

RESULT 14

US-09-047-026A-15
Sequence 15, Application US/09047026A
Patent No. 5989897
GENERAL INFORMATION:
APPLICANT: Pillus, Lorraine
APPLICANT: Clarke, Astrid
APPLICANT: Lowell, Joana
APPLICANT: Jacobson, Sandra
APPLICANT: Reitsnyder, Cheryl
TITLE OF INVENTION: Yeast Silencing Genes, Proteins and
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,026A
FILING DATE: 24-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,375
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 1-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-09-047-026A-15

Query Match 31.3%; Score 31; DB 2; Length 24;
Best Local Similarity 37.5%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 3 PGHERMGRGRTSSKEL 18
| | | | | | | | | | | | | | | | | |
DB 8 PDYQROGLGRALLEHL 23

RESULT 15

US-08-196-945-9
Sequence 9, Application US/08196945
Patent No. 5563032
GENERAL INFORMATION:
APPLICANT: FIELDS, HOWARD A.
APPLICANT: KHUDYAKOV, YURI E.
APPLICANT: FAVOROV, MICHAEL O.
TITLE OF INVENTION: MOSAIC POLYPEPTIDE AND METHODS FOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Bldg.,

STREET: 127 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,945
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-196-945-9

Query Match 30.8%; Score 30.5; DB 1; Length 21;
Best Local Similarity 45.0%; Pred. No. 52;
Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NVPGH-ERMGRGRTSKELA 19
| | | | : | | | : | |
Db 2 NOPGHLPGLGEIRSPAPPLA 21

RESULT 16
US-07-965-667A-10
Sequence 10 Application US/07965667A
Patent No. 5736315
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
APPLICANT: Favorov, Michael O.
APPLICANT: Khudyakov, Yuri E.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: ANTI-HEPATITIS E VIRUS ACTIVITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 133 Carnegie Way, N.W., Suite 400
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,667A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414,022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-965-667A-10

Query Match 30.8%; Score 30.5; DB 1; Length 21;
Best Local Similarity 45.0%; Pred. No. 52;
Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NVPGH-ERMGRGRTSKELA 19
| | | | : | | | : | |
Db 2 NOPGHLPGLGEIRSPAPPLA 21

RESULT 17
US-08-484-819-10
Sequence 10 Application US/08484819
Patent No. 6022685
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
APPLICANT: Favorov, Michael O.
APPLICANT: Khudyakov, Yuri E.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: ANTI-HEPATITIS E VIRUS ACTIVITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 133 Carnegie Way, N.W., Suite 400
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,819
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,667
FILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414,022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-819-10

Query Match 30.8%; Score 30.5; DB 3; Length 21;
Best Local Similarity 45.0%; Pred. No. 52;
Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NVPGH-ERMGRGRTSKELA 19
| | | | : | | | : | |
Db 2 NOPGHLPGLGEIRSPAPPLA 21

RESULT 18
PCT-US93-10197-10
; Sequence 10, Application PC/TUS9310197
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: ANTI-HEPATITIS E VIRUS ACTIVITY"
; NUMBER OF SEQUENCES: 20
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 EPO
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10197
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,667
; FILING DATE: 21-OCT-1992
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-10197-10

Query Match 30.8%; Score 30.5; DB 5; Length 21;
Best Local Similarity 45.0%; Pred. No. 52;
Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 NVPGH-ERMGRGRTSSKELA 19
Db 2 NPGHLAGELRPSAPPLA 21

RESULT 19
US-08-651-818A-20
; Sequence 20, Application US/08651818A
; Patent No. 5948889
; GENERAL INFORMATION:
; APPLICANT: de Boer, Plet A.J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
; TITLE OF INVENTION: ANTIMICROBIALS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,818A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: CASE-02249
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid

; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-651-818A-20

Query Match 30.3%; Score 30; DB 2; Length 14;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 NVPGHERMGRG 11
Db 3 SMTGGQOMGRG 13

RESULT 20
US-08-722-806A-10
; Sequence 10, Application US/08722806A
; Patent No. 5981247
; GENERAL INFORMATION:
; APPLICANT: Hagedorn, Curt H.
; APPLICANT: Al, Reinoldus H.
; TITLE OF INVENTION: Recombinant Hepatitis C Virus RNA
; TITLE OF INVENTION: Replicase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,806A
; FILING DATE: 27-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004383
; FILING DATE: 27-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenlee, Lorraine L.
; REGISTRATION NUMBER: 27,894
; REFERENCE/DOCKET NUMBER: 76-9505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-722-806A-10

Query Match 30.3%; Score 30; DB 2; Length 14;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 NVPGHERMGRG 11
Db 3 SMTGGQOMGRG 13

RESULT 21
US-09-184-826-20
; Sequence 20, Application US/09184826
; Patent No. 6248543
; GENERAL INFORMATION:
; APPLICANT: de Boer, Plet A.J.

APPLICANT: Hale, Cynthia A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
TITLE OF INVENTION: ANTIMICROBIALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,826
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: CASE-02249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-184-826-20
Query Match
Best Local Similarity 30.3%; Score 30; DB 4; Length 14;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 1 NVPGHERMGRG 11
Db 3 SMTGGQGMGRG 13
RESULT 22
US-09-337-028-10
Sequence 10, Application US/09337028
Patent No. 6248589
GENERAL INFORMATION:
APPLICANT: Hagedorn, Curt H.
APPLICANT: Al, Reinholdus H.
TITLE OF INVENTION: Recombinant Hepatitis C Virus RNA Replicase
FILE REFERENCE: RECOM HEPATITIS C VIRUS RNA REPLICASE
CURRENT APPLICATION NUMBER: US/09/337,028
CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: US 60/004,383
EARLIER FILING DATE: 1995-09-27
EARLIER APPLICATION NUMBER: US 08/722, 806
EARLIER FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-337-028-10
Query Match
Best Local Similarity 30.3%; Score 30; DB 4; Length 14;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 1 NVPGHERMGRG 11
Db 3 SMTGGQGMGRG 13

Db 3 SMTGGQGMGRG 13
RESULT 23
US-09-597-877-10
Sequence 10, Application US/09597877
Patent No. 6461845
GENERAL INFORMATION:
APPLICANT: Hagedorn, Curt H.
TITLE OF INVENTION: Recombinant Hepatitis C Virus RNA Replicase
FILE REFERENCE: 76-95B
CURRENT APPLICATION NUMBER: US/09/597,877
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 60/004,383
PRIOR FILING DATE: 1995-09-27
PRIOR APPLICATION NUMBER: 08/722,806
PRIOR FILING DATE: 1996-09-27
PRIOR APPLICATION NUMBER: 09/337,028
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence of the cloning site in pET-11a where the
OTHER INFORMATION: 5' end of the PCR amplified NS5b gene was
US-09-597-877-10
Query Match
Best Local Similarity 30.3%; Score 30; DB 4; Length 14;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 1 NVPGHERMGRG 11
Db 3 SMTGGQGMGRG 13
RESULT 24
US-08-310-912A-95
Sequence 95, Application US/08310912A
Patent No. 5981730
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,912A
FILING DATE: September 22, 1994

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/254001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
08-310-912A-95

Query Match 29.3%; Score 29; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VPGRH 7
||| |
DB 3 VPGHTR 8

RESULT 25

US-08-841-089-95
Sequence 95, Application US/08841089
Patent No. 6127607

GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskiewicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/841,089
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-841-089-95

Query Match 29.3%; Score 29; DB 3; Length 10;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VPGRH 7
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DB 3 VPGHTR 8

Search completed: March 14, 2003, 16:07:34
Job time : 38 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:02:37 ; Search time 36 Seconds
(without alignments)
70.327 Million cell updates/sec

Title: us-09-674-913a-1

Sequence: 1 NPGHERMGRGRTSSKELA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 320064

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	99	100.0	25	19	AAV20219
3	82.5	83.3	19	22	AAV56391
4	63	63.6	14	22	AAV56391
5	58	58.6	12	21	AAV56391
6	52.5	52.5	17	21	AAV56391
7	47	47.5	10	18	AAV18633
8	47	47.5	10	18	AAV18633
9	47	47.5	10	18	AAV18633
10	41	41.4	15	21	AAV56391

11	33.5	33.8	24	21	AAV48661	Human zvegf4 pepti
12	33.5	33.8	24	22	AAV56391	Human zvegf4 pepti
13	33.5	33.8	24	23	AAV56391	Human zvegf4 pepti
14	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
15	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
16	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
17	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
18	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
19	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
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25	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
26	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
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33	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
34	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
35	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
36	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
37	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
38	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
39	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
40	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
41	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
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44	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
45	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
46	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
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49	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
50	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
51	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
52	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
53	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
54	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
55	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
56	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
57	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
58	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
59	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
60	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
61	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
62	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
63	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
64	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
65	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
66	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
67	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
68	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
69	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
70	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
71	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
72	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
73	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
74	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
75	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
76	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
77	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
78	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
79	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
80	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
81	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
82	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti
83	33.3	33.3	20	22	AAV56391	Human zvegf4 pepti

84	28	28.3	14	22	AA655341	Human interleukin-1
85	28	28.3	15	18	AAW30950	Timothy grass poll
86	28	28.3	15	20	AAV22935	Peptide derived fr
87	28	28.3	15	20	AAV22953	Synthetic peptide
88	28	28.3	16	15	AAW52169	Human light chain
89	28	28.3	20	21	AAV50993	Potato pr17-WT pro
90	28	28.3	20	22	AAW80668	Human peptide #134
91	28	28.3	20	22	AAW85140	Sequence of a synt
92	28	28.3	20	22	AAW85141	Sequence of a synt
93	28	28.3	20	22	AAW85142	Sequence of a synt
94	28	28.3	21	22	AAW06773	Human dual-specific
95	28	28.3	22	20	AAV22922	Flagrin derived a
96	28	28.3	22	20	AAV22942	Synthetic peptide
97	28	28.3	22	20	AAV22947	Synthetic peptide
98	28	28.3	23	23	AAE19024	Human ghrelin pept
99	28	28.3	23	23	AAW91208	Insulin and insuli
100	28	28.3	24	22	AAW91208	ESBP mutated fragm
101	28	28.3	25	20	AAV09077	Novel human diagno
102	27	27.3	8	18	AAW34356	PKB substrate #3.
103	27	27.3	8	21	AAV58257	Protein kinase B (
104	27	27.3	10	18	AAW15659	Platelet aggregati
105	27	27.3	10	22	AAW94455	Human complementar
106	27	27.3	10	22	AAW97174	Human complementar
107	27	27.3	10	22	AAW85559	Saccharomyces cere
108	27	27.3	10	22	AAW85565	Saccharomyces cere
109	27	27.3	10	22	AAW85579	Saccharomyces cere
110	27	27.3	10	22	AAW86075	Saccharomyces cere
111	27	27.3	10	22	AAW61354	Anti-thrombotic cy
112	27	27.3	11	17	AAW98330	Interleukin-1 prod
113	27	27.3	11	18	AAW34354	PKB substrate #1.
114	27	27.3	11	21	AAV93508	Crosslink peptide
115	27	27.3	11	21	AAV93508	Peptide substrate
116	27	27.3	11	21	AAV93508	Crosslink peptide.
117	27	27.3	11	21	AAV95259	Crosspeptide amino
118	27	27.3	11	21	AAV85173	Phosphoserine AKT
119	27	27.3	11	21	AAV54015	GSK3-derived pepti
120	27	27.3	11	21	AAV58261	Crosslink peptide
121	27	27.3	11	22	AAW06068	Crosslink peptide
122	27	27.3	11	22	AAW97899	Protein kinase B a
123	27	27.3	11	22	AAE04940	Nuclear Dbp2-relat
124	27	27.3	11	22	AAU02106	Human phosphorilat
125	27	27.3	11	22	AAW97048	MSK substrate pept
126	27	27.3	11	22	AAW74330	Crosslink peptide
127	27	27.3	12	17	AAW98331	Interleukin-1 prod
128	27	27.3	12	23	AAU07498	Protein kinase B s
129	27	27.3	13	19	AAW56812	Enzyme inhibitor p
130	27	27.3	13	23	AAW61650	Human G protein-co
131	27	27.3	14	22	AAW98433	Human peptide #170
132	27	27.3	14	22	AAW09503	Human histone frag
133	27	27.3	15	15	AAW47738	HIV epitope #71
134	27	27.3	15	20	AAW40703	A3 derivative #24.
135	27	27.3	15	21	AAW30042	Scaffold protein S
136	27	27.3	16	15	AAW9507	Hydrophilic linker
137	27	27.3	16	15	AAW9507	Bovine chondroelek
138	27	27.3	16	23	AAE13272	Linker peptide to
139	27	27.3	17	20	AAW85631	Antigenic epitope
140	27	27.3	18	20	AAE14576	Human JF46726 pep
141	27	27.3	20	15	AAW75668	Human plasmin N-ce
142	27	27.3	20	21	AAW81350	Streptavidin displ
143	27	27.3	21	20	AAW36587	Fragment of human
144	27	27.3	21	23	AAW83068	M13 segment of smo
145	27	27.3	22	23	AAW49321	HIV-1 gp120 V3 loo
146	27	27.3	22	23	AAW22732	Human dual-specific
147	27	27.3	23	22	AAW11033	Novel human diagno
148	27	27.3	24	14	AAW41126	HCV peptide Xxb-1
149	27	27.3	25	21	AAV09074	EGFP mutated fragm
150	27	27.3	25	21	AAV52526	House dust mite al
151	27	27.3	25	22	AAU01686	Human secreted pro
152	27	27.3	25	23	AAU96350	Der HMW-map polype
153	26	26.3	16	19	AAW76431	PKB substrate 3-4 of
154	26	26.3	7	18	AAW34367	PKB substrate #14.
155	26	26.3	7	21	AAV93522	Peptide substrate
156	26	26.3	7	23	AAV95272	Crosslink-derived
	26	26.3	7	23	AAW34942	Human bone marrow

Human complementar
Human complementar
Human complementar
Human complementar
Saccharomyces cere
Saccharomyces cere
Saccharomyces cere
Human secreted pro
Phosphorylated dhl
HIV-2 strain ROD V
Anti-methenyltetra
Macrophage-colony
Methenyltetrahydro
Epstein-Barr virus
Epstein-Barr virus
Chenopodium album
Fragment of pertus
Human peptide #823
Human peptide #823
Human Interleukin-
Human thyrocalcilo
HER2/NEU DR superm
Human protein phos
Human leucocyte an
Human light chain
Human light chain
Macaque histatin-1
Macaque histatin 1
Peptide #9360 enco
Protein #7556 enco
Human brain expres
Human bone marrow
Peptide #7065 enco
Peptide #9690 enco
Human peptide enco
Insulin/insulin-11
Insulin/insulin-11
Methylated Smb hom
S lividans Desr re
Laminin A chain de
Macaque histatin-1
Peptide cfc3, base
Macaque histatin 1
BAX mutant peptide
HIV-1 clinical str
Bovine oncostatin
Peptide sequence o
Mouse BAX amino ac
Rat BAX amino acid
Human matrix metal
OEG antibody epito
Feline FlkFp35 pro
Novel human diagno
Peptide #1442 enco
Peptide #1484 enco
Protein #1415 enco
Human brain expres
Human bone marrow
Peptide #1432 enco
Peptide #1471 enco
Peptide #1407 enco
Human peptide enco
Macaque histatin-1
Macaque histatin-1
Peptide #2607 enco
Human brain expres
Human peptide enco
HCV peptide xxd-1
Novel human diagno
NDF- α h2a2(1-241)
Isolated peptide f
Vitronectin fragme
UPAR targeting seq

230	25.5	25.8	25	19	AAW60534	Sequence joint bet	303	25	25.3	15	22	ABP25386	HIV-1 epitope #40.
231	25.5	25.8	25	19	AAU93714	Dental product bon	304	25	25.3	15	22	ABP25388	HIV-1 epitope #42.
232	25.5	25.8	25	23	AAO20364	Peptide of matrix	305	25	25.3	15	23	ABP47084	Human Blys binding
233	25	25.3	25	22	AAAB0684	Human glandular ka	306	25	25.3	15	23	AAU78647	Synthetic peptide
234	25	25.3	25	13	AAAR7705	Peptide (205) inh1	307	25	25.3	15	23	AAE16617	Human KCNO5 immuno
235	25	25.3	25	17	AAW49339	Human leucocyte an	308	25	25.3	16	15	AAAR2127	Mouse light chain
236	25	25.3	25	9	AAW83400	Type II collagen m	309	25	25.3	16	16	AAAR70345	NF-AT transcriptio
237	25	25.3	25	9	AAAB19776	Human leucocyte p	310	25	25.3	16	16	AAAR83275	HIV principal neut
238	25	25.3	25	21	AAE18745	Human leucocyte an	311	25	25.3	16	16	AAAR63559	Peptide MCL3 deri
239	25	25.3	25	9	AAU71305	Human MHC class I	312	25	25.3	16	21	AAAY65552	Human NF-ATc1 anti
240	25	25.3	25	9	AAU71395	Human MHC class I	313	25	25.3	16	21	AAAY73152	Human NF-ATc1 anti
241	25	25.3	25	9	AAU71596	Human MHC class I	314	25	25.3	16	22	AAU12486	Human HIV-1 Th-CTL
242	25	25.3	25	9	AAU71698	Human MHC molecule	315	25	25.3	16	22	AAAB6484	Human NF-AT peptid
243	25	25.3	25	9	AAU71736	Human MHC molecule	316	25	25.3	16	23	AAAE21546	Human NF-ATc anti
244	25	25.3	25	10	AAAR8329	Interleukin-1 prod	317	25	25.3	17	18	AAAW6755	Thrombopoietin rec
245	25	25.3	25	10	AAAG95908	Human complementar	318	25	25.3	17	18	AAAW09604	Thrombopoietin rec
246	25	25.3	25	10	AAAG83516	Arbidopsis thalla	319	25	25.3	17	20	AAAY64476	Fragment of human
247	25	25.3	25	10	AAAG84361	Arbidopsis thalla	320	25	25.3	17	22	AAAB28215	Human peptide #866
248	25	25.3	25	10	AAAG86859	Saccharomyces cere	321	25	25.3	17	22	AAAB33390	Peptide #896 encod
249	25	25.3	25	10	AAAG87824	Saccharomyces cere	322	25	25.3	17	22	AAAB18849	Protein #848 encod
250	25	25.3	25	10	AAAG87825	Saccharomyces cere	323	25	25.3	17	22	AAU25974	Human thrombopoiet
251	25	25.3	25	10	AAU71174	Human MHC class I	324	25	25.3	17	22	AAAM54175	Human brain expres
252	25	25.3	25	10	AAU71268	Human MHC class I	325	25	25.3	17	22	AAAM65659	Human bone marrow
253	25	25.3	25	10	AAU71376	Human MHC class I	326	25	25.3	17	22	AAAM14442	Peptide #876 encod
254	25	25.3	25	10	AAU71452	Human MHC molecule	327	25	25.3	17	22	AAAM26855	Peptide #892 encod
255	25	25.3	25	10	AAU71571	Human MHC class I	328	25	25.3	17	22	AAAM02169	Peptide #851 encod
256	25	25.3	25	10	AAU71591	Human MHC class I	329	25	25.3	17	22	AAAB67966	l25 peptide derive
257	25	25.3	25	10	AAU71651	Human MHC class I	330	25	25.3	17	22	AAAB48157	Human MCH receptor
258	25	25.3	25	11	AAAW09224	Repeat peptide use	331	25	25.3	17	23	AAAG36221	Human peptide enco
259	25	25.3	25	11	AAAR8439	Peptide with cell	332	25	25.3	17	23	AAAG10745	Human RGS18 N-term
260	25	25.3	25	11	AAAW59794	Tobacco PAPd repe	333	25	25.3	17	23	AAAB74819	Nuclear protein nu
261	25	25.3	25	11	AAAY51894	Protocol X peptide	334	25	25.3	18	21	AAAY97251	M68 TNFR-like prot
262	25	25.3	25	11	AAAY80341	Synthetic bioelast	335	25	25.3	18	22	AAAM60008	Human brain expres
263	25	25.3	25	11	AAAY80343	Synthetic bioelast	336	25	25.3	18	22	AAAM72608	Human bone marrow
264	25	25.3	25	12	AAAW07228	HIV-1 group O stra	337	25	25.3	18	23	AAAB84980	Insulin/insulin-li
265	25	25.3	25	12	AAAR86441	Peptide with cell	338	25	25.3	19	19	AAAM61509	Peptide cec5, base
266	25	25.3	25	12	AAAM50247	T7-tag epitope. S	339	25	25.3	19	19	AAAM61514	Peptide ctf, based
267	25	25.3	25	12	AAAM50247	Peptide 30P used I	340	25	25.3	19	23	AAAB08198	Human protein zero
268	25	25.3	25	13	AAAM57036	Enzyme inhibitor P	341	25	25.3	19	17	AAAR8306	p21WAF1 peptide 6.
269	25	25.3	25	13	AAAM56808	Enzyme inhibitor P	342	25	25.3	20	18	AAAM44229	Human p21waf1 frag
270	25	25.3	25	13	AAAB39635	Anti-IL12 antibody	343	25	25.3	20	21	AAAB13671	C. trachomatis OMC
271	25	25.3	25	13	AAAG73192	Protease binding s	344	25	25.3	20	21	AAAB13672	C. trachomatis OMC
272	25	25.3	25	13	AAAG73314	Protease indicator	345	25	25.3	20	21	AAAB18498	Peptide substrate
273	25	25.3	25	13	AAU98796	Bovine Ribosomal P	346	25	25.3	20	21	AAAY98349	Alpha D peptide de
274	25	25.3	25	13	ABP47170	Human Blys binding	347	25	25.3	20	22	AAAG83239	Chlamydia trachoma
275	25	25.3	25	14	AAAR8436	Peptide with cell	348	25	25.3	20	22	AAAG83240	Chlamydia trachoma
276	25	25.3	25	14	AAAM6171	Peptide 30M used I	349	25	25.3	20	23	AAAG62838	Ligand/receptor sp
277	25	25.3	25	14	AAAG7536	Human peptide #811	350	25	25.3	20	23	AAAG62839	DNA binding peptid
278	25	25.3	25	14	AAAM8228	Human peptide #150	351	25	25.3	20	23	AAO17408	DNA binding peptid
279	25	25.3	25	14	AAAM8685	Human peptide #196	352	25	25.3	20	23	AAO17416	Chlamydia peptide
280	25	25.3	25	14	AAU68487	Human Breast cance	353	25	25.3	20	23	AAAB94210	Chlamydia peptide
281	25	25.3	25	14	AAAM00425	Human protein frag	354	25	25.3	20	23	AAAB94211	Chlamydia peptide
282	25	25.3	25	14	AAAM00426	Human protein frag	355	25	25.3	21	19	AAAY21024	Human glial fibrin
283	25	25.3	25	14	AAAG73313	Protease indicator	356	25	25.3	21	19	AAAM46342	Amino acid sequenc
284	25	25.3	25	15	AAAM5403	Helper T-cell clas	357	25	25.3	21	20	AAAY22147	Peptide used for F
285	25	25.3	25	15	AAAM5340	Helper T-cell clas	358	25	25.3	21	21	AAAB37204	Repressivus-1 ICP2
286	25	25.3	25	15	AAAM5205	Helper T-cell clas	359	25	25.3	21	22	AAAB35273	Human dual specifi
287	25	25.3	25	15	AAAM5215	Helper T-cell pept	360	25	25.3	21	22	AAAB83070	Partial amino acid
288	25	25.3	25	15	AAAM62035	PDZ3 specific pept	361	25	25.3	22	20	AAAY00773	Mouse tag7 clone p
289	25	25.3	25	15	AAAY3153	HIV-derived MHC cI	362	25	25.3	22	21	AAAY98802	WT1 derived immuno
290	25	25.3	25	15	AAAY3154	HIV-derived MHC cI	363	25	25.3	22	22	AAU68901	Human WT1's tumou
291	25	25.3	25	15	AAAB24697	HIV DR super motif	364	25	25.3	22	22	AAAG62134	Human WT1 immunog
292	25	25.3	25	15	AAAB24698	HIV DR super motif	365	25	25.3	22	23	AAAG33371	Human WT1 immunog
293	25	25.3	25	15	AAAB24743	HIV DR super motif	366	25	25.3	22	17	AAAM07330	C-terminus of myc-
294	25	25.3	25	15	AAAB24745	HIV DR super motif	367	25	25.3	24	21	AAAB51768	Human secreted pro
295	25	25.3	25	15	AAAB25067	HIV DR supermotif	368	25	25.3	25	12	AAAR12282	Parvovirus B19 epi
296	25	25.3	25	15	AAAB25068	HIV DR supermotif	369	25	25.3	25	15	AAAR47398	PDGf-activitv-dlsp
297	25	25.3	25	15	AAAB25255	HIV HLA-DR binding	370	25	25.3	25	20	AAAY09085	E6B8 mutated fragm
298	25	25.3	25	15	AAAB25257	HIV HLA-DR binding	371	25	25.3	25	20	AAAY09086	E6B8 mutated fragm
299	25	25.3	25	15	AAAB25274	HIV-derived DR-sup	372	25	25.3	25	20	AAAY09087	E6B8 mutated fragm
300	25	25.3	25	15	AAAB25275	HIV-derived DR-sup	373	25	25.3	25	20	AAAY09083	E6B8 mutated fragm
301	25	25.3	25	15	AAAB25332	HTL cadidate epitc	374	25	25.3	25	20	AAAY09084	E6B8 mutated fragm
302	25	25.3	25	15	AAAB25334	HTL cadidate epitc	375	25	25.3	25	20	AAAY09082	E6B8 mutated fragm

522	24	24.2	18	21	AAV95915	Hypothetical signa
523	24	24.2	18	21	AAI17119	Calmodulin antagon
524	24	24.2	18	22	AAI80806	DtxR homologue lig
525	24	24.2	18	22	AAI61816	Try59 polypeptide
526	24	24.2	18	22	AAI55529	Peptide linker #3.
527	24	24.2	18	22	AAI57786	Flexible polylinke
528	24	24.2	18	22	AAI57786	Flexible polylinke
529	24	24.2	18	22	AAI3197	Calmodulin antagon
530	24	24.2	19	14	AAI3042	N-terminal fragmen
531	24	24.2	19	15	AAI58355	Porcine parvovirus
532	24	24.2	19	15	AAI66629	HSV-2 glycoprotein
533	24	24.2	19	19	AAI61508	Peptide circ4, base
534	24	24.2	19	20	AAI27164	Mouse STRL peptide
535	24	24.2	19	21	AAI98289	Alpha D peptide de
536	24	24.2	19	21	AAI98290	Alpha D peptide de
537	24	24.2	19	22	AAI47234	hmf1 Mitofusin GT
538	24	24.2	19	23	AAI17770	Human beta-defensi
539	24	24.2	19	23	AAI93571	Granulocyte-colony
540	24	24.2	19	23	AAI73575	Vascular endotheli
541	24	24.2	20	13	AAI24872	Sequence of a pep
542	24	24.2	20	18	AAI26360	Erythropoietin rec
543	24	24.2	20	18	AAI13713	Erythropoietin rec
544	24	24.2	20	18	AAI26696	Toxoplasma gondii
545	24	24.2	20	18	AAI27027	Monomer subunit of
546	24	24.2	20	19	AAI71650	Smooth muscle myos
547	24	24.2	20	20	AAI26295	Peptide comprising
548	24	24.2	20	21	AAI23112	penut wild-type A
549	24	24.2	20	21	AAI33561	5/20 native Ara h
550	24	24.2	20	21	AAI13297	Caenothabditis ele
551	24	24.2	20	22	AAI28788	Peptide #1439 enco
552	24	24.2	20	22	AAI33975	Peptide #1481 enco
553	24	24.2	20	22	AAI19414	Protein #1413 enco
554	24	24.2	20	22	AAI54738	Human brain expres
555	24	24.2	20	22	AAI67132	Human bone marrow
556	24	24.2	20	22	AAI14896	Peptide #1430 enco
557	24	24.2	20	22	AAI27432	Peptide #1469 enco
558	24	24.2	20	22	AAI04774	Native anaphylacti
559	24	24.2	20	22	AAI05099	Anaphylactic peanu
560	24	24.2	20	22	AAI05375	R1 and R2 peptide
561	24	24.2	20	22	AAI02723	Peptide #1405 enco
562	24	24.2	20	22	AAI17161	DAPPI immunogenic
563	24	24.2	20	22	AAI50818	Turkey protein cal
564	24	24.2	20	23	AAI6794	Human peptide enco
565	24	24.2	20	23	AAI17404	DNA binding peptid
566	24	24.2	20	23	AAI090347	Insulin/Insulin-1i
567	24	24.2	21	13	AAI27074	Recombinant xylana
568	24	24.2	21	19	AAI97205	N-terminal fragmen
569	24	24.2	21	22	AAI22432	Novel human diagno
570	24	24.2	21	22	AAI55702	Peptide associated
571	24	24.2	21	22	AAI57959	Tat-CLASPcarboxyl
572	24	24.2	21	22	AAI57959	Tat-CLASPcarboxyl
573	24	24.2	21	23	AAI88608	Insulin/Insulin-1i
574	24	24.2	21	23	AAI1156	Hirulog-17. Synth
575	24	24.2	22	15	AAI47613	Bombesin-like pept
576	24	24.2	22	15	AAI47613	Bombesin-like pept
577	24	24.2	22	20	AAI22160	Human BS135 protei
578	24	24.2	22	21	AAI13646	C. trachomatis pmp
579	24	24.2	22	22	AAI87914	Human Immunoe/haema
580	24	24.2	22	22	AAI63214	PE17b expression
581	24	24.2	22	23	AAI01837	Breast tissue libt
582	24	24.2	22	23	AAI94185	Chlamydia peptide
583	24	24.2	23	15	AAI58462	TSAR binding domai
584	24	24.2	23	17	AAI89957	Rabbit eif-4-gamma
585	24	24.2	23	20	AAI36404	Fragment of human
586	24	24.2	23	20	AAI01040	Methylated SMD hom
587	24	24.2	23	21	AAI81936	Kemptide phospho
588	24	24.2	23	22	AAI829178	Peptide #1829 enco
589	24	24.2	23	22	AAI83434	Peptide #1840 enco
590	24	24.2	23	22	AAI19755	Protein #1754 enco
591	24	24.2	23	22	AAI55131	Human bone marrow
592	24	24.2	23	22	AAI65753	Human brain expres
593	24	24.2	23	22	AAI15337	Peptide #1771 enco
594	24	24.2	23	22	AAI27814	Peptide #1851 enco
595	24	24.2	23	22	AAI03096	Peptide #1778 enco
596	24	24.2	23	22	AAI37119	Human peptide enco
597	24	24.2	24	18	AAI23495	Antibacterial and/
598	24	24.2	24	19	AAI44187	Mateate cis-trans
599	24	24.2	24	20	AAI39412	Human Interleukin-
600	24	24.2	24	21	AAI18711	Synthetic peptide
601	24	24.2	24	21	AAI18711	N-terminus of Haem
602	24	24.2	24	23	AAI17774	Human beta-defensi
603	24	24.2	24	23	AAI78012	Human Interleukin
604	24	24.2	25	14	AAI41074	HIV-1 partial V3 l
605	24	24.2	25	16	AAI68759	Cytotoxic T lympho
606	24	24.2	25	18	AAI32896	HIV pol protein ep
607	24	24.2	25	19	AAI75039	Fragment of human
608	24	24.2	25	22	AAI64846	Human brain expres
609	24	24.2	25	22	AAI30911	Amino acid sequenc
610	24	24.2	25	23	AAI68885	HIV-1 p21 peptide
611	24	24.2	25	23	AAI62629	Eubacterial DnaE1
612	24	24.2	25	23	AAI67332	Omega-conopeptide
613	24	24.2	25	23	AAI78615	Human Bad peptide
614	24	24.2	25	23	AAI70911	Human Bad peptide
615	24	24.2	25	23	AAI80510	Histone 2A-derived
616	24	24.2	25	16	AAI43620	S. lividans protea
617	24	24.2	16	20	AAI42046	Immunospecific pep
618	24	24.2	18	22	AAI27366	Human ADP1 tryptic
619	24	24.2	22	22	AAI31977	Novel bone marrow
620	24	24.2	6	4	AAI30272	Novel human secret
621	24	24.2	5	19	AAI87141	Sequence of AAs 32
622	24	24.2	7	15	AAI48438	Peptide determined
623	24	24.2	7	15	AAI48438	Histogranin deriva
624	24	24.2	7	20	AAI42046	Histogranin deriva
625	24	24.2	7	21	AAI1853	Rheumatoid arthrit
626	24	24.2	8	15	AAI48435	Alpha-MSH analoge
627	24	24.2	8	15	AAI48474	Histogranin deriva
628	24	24.2	8	17	AAI05711	Histogranin deriva
629	24	24.2	8	19	AAI79116	Minimal motif #8.
630	24	24.2	8	19	AAI66163	Gly-ala polymer of
631	24	24.2	8	21	AAI08149	MSH-receptor subty
632	24	24.2	9	14	AAI43436	Peptide modulating
633	24	24.2	9	15	AAI48432	R/S5A epitope 84.
634	24	24.2	9	15	AAI48471	Histogranin deriva
635	24	24.2	9	15	AAI48492	Histogranin deriva
636	24	24.2	9	15	AAI57718	Histogranin deriva
637	24	24.2	9	15	AAI57720	Peptide (218) inh
638	24	24.2	9	15	AAI57707	Peptide (220) inh
639	24	24.2	9	15	AAI57709	Peptide (209) inh
640	24	24.2	9	15	AAI57693	Peptide (193) inh
641	24	24.2	9	17	AAI49388	Human leucocyte an
642	24	24.2	9	17	AAI12598	SH2 binding peptid
643	24	24.2	9	17	AAI12599	SH2 binding peptid
644	24	24.2	9	19	AAI66164	MSH-receptor subty
645	24	24.2	9	20	AAI07472	Mouse MMAC1 gene b
646	24	24.2	9	21	AAI96715	Human E3 ubiquitin
647	24	24.2	9	22	AAI6255	Influenza virus im
648	24	24.2	10	15	AAI38353	p53-derived HLA-bi
649	24	24.2	10	15	AAI48429	Histogranin deriva
650	24	24.2	10	15	AAI48437	Histogranin deriva
651	24	24.2	10	15	AAI48468	Histogranin deriva
652	24	24.2	10	15	AAI48476	Histogranin deriva
653	24	24.2	10	17	AAI12579	SH2 binding peptid
654	24	24.2	10	17	AAI12570	SH2 binding peptid
655	24	24.2	10	18	AAI32644	Human platelet gly
656	24	24.2	10	18	AAI32644	Human platelet gly
657	24	24.2	10	19	AAI17770	Minotopo capable o
658	24	24.2	10	19	AAI17773	Minotopo capable o
659	24	24.2	10	20	AAI55308	CD34 antigen antiq
660	24	24.2	10	20	AAI45934	Immunogenic peptid
661	24	24.2	10	20	AAI46996	Immunogenic peptid
662	24	24.2	10	21	AAI06153	sceV 9A4 clone 23A
663	24	24.2	10	21	AAI06153	Human haematopoiet
664	24	24.2	10	22	AAI23947	HIV A11 motif vif
665	24	24.2	10	22	AAI60167	Human complementar
666	24	24.2	10	22	AAI60167	Human complementar
667	24	24.2	10	22	AAI33833	Human complementar

668	23	23.2	10	22	AAG95776	Human complementtar	741	23	23.2	14	15	AAR48422	Histogranin deriva
669	23	23.2	10	22	AAG95827	Human complementtar	742	23	23.2	14	15	AAR48461	Histogranin deriva
670	23	23.2	10	22	AAG95878	Human complementtar	743	23	23.2	14	15	AAR48491	Histogranin deriva
671	23	23.2	10	22	AAG97172	Human complementtar	744	23	23.2	14	15	AAR48494	Histogranin deriva
672	23	23.2	10	22	AAG97722	Arabidopsis thalia	745	23	23.2	14	20	AAV30321	Potential T cell e
673	23	23.2	10	22	AAG83853	Arabidopsis thalia	746	23	23.2	14	20	AAV06546	Hepatocellular car
674	23	23.2	10	22	AAG83855	Arabidopsis thalia	747	23	23.2	14	20	AAV03194	Amino acid sequenc
675	23	23.2	10	22	AAG83857	Arabidopsis thalia	748	23	23.2	14	21	AAB20728	High mobility grou
676	23	23.2	10	22	AAG83859	Arabidopsis thalia	749	23	23.2	14	21	AAV66426	H1A-A2-binding HIV
677	23	23.2	10	22	AAG83883	Arabidopsis thalia	750	23	23.2	14	22	AAV96782	Human peptide #57
678	23	23.2	10	22	AAG83885	Arabidopsis thalia	751	23	23.2	14	22	AAV96896	Human peptide #171
679	23	23.2	10	22	AAG83887	Arabidopsis thalia	752	23	23.2	14	22	AAV97054	Human peptide #529
680	23	23.2	10	22	AAG85381	Saccharomyces cere	753	23	23.2	14	22	AAV97903	Human peptide #117
681	23	23.2	10	22	AAG85385	Saccharomyces cere	754	23	23.2	14	22	AAV97967	Human peptide #124
682	23	23.2	10	22	AAG86466	Saccharomyces cere	755	23	23.2	14	22	AAV98195	Human peptide #147
683	23	23.2	10	22	AAG86482	Saccharomyces cere	756	23	23.2	14	22	AAV98233	Human peptide #150
684	23	23.2	10	22	AAG86484	Saccharomyces cere	757	23	23.2	14	22	AAV98534	Human peptide #180
685	23	23.2	10	22	AAG86492	Saccharomyces cere	758	23	23.2	14	22	AAV00660	Human PC-LECTIN ex
686	23	23.2	10	22	AAG86597	Saccharomyces cere	759	23	23.2	14	22	AAB73315	Human PC-LECTIN ex
687	23	23.2	10	22	AAG86858	Saccharomyces cere	760	23	23.2	14	22	AAB88025	CDb6 peptide CDb6a
688	23	23.2	10	22	AAG86858	ps3 epitope H1A-A3	761	23	23.2	14	22	AAV59415	Human Class I HLA-
689	23	23.2	11	15	AAR48423	Histogranin deriva	762	23	23.2	15	7	AAV60481	Epstein-Barr virus
690	23	23.2	11	15	AAR48434	Histogranin deriva	763	23	23.2	15	10	AAV90199	Antigenic peptide
691	23	23.2	11	15	AAR48462	Histogranin deriva	764	23	23.2	15	13	AAV25058	Synthetic random c
692	23	23.2	11	15	AAR48473	Histogranin deriva	765	23	23.2	15	13	AAV47735	HIV epitope #68
693	23	23.2	11	16	AAW21338	Glucagon precursor	766	23	23.2	15	15	AAV48380	Histogranin . Bos
694	23	23.2	11	21	AAV09394	Hepatitis GB virus	767	23	23.2	15	15	AAV48381	Histogranin deriva
695	23	23.2	11	22	ABP14143	HIV A02 super moti	768	23	23.2	15	15	AAV48382	Histogranin deriva
696	23	23.2	11	22	ABP1562	HIV B27 super moti	769	23	23.2	15	15	AAV48383	Histogranin deriva
697	23	23.2	11	23	AAE23345	Human GSK3alpha de	770	23	23.2	15	15	AAV48385	Histogranin deriva
698	23	23.2	12	15	AAV45675	Apo B heparin bind	771	23	23.2	15	15	AAV48386	Histogranin deriva
699	23	23.2	12	15	AAV48391	Histogranin deriva	772	23	23.2	15	15	AAV48387	Histogranin deriva
700	23	23.2	12	15	AAV48392	Histogranin deriva	773	23	23.2	15	15	AAV48388	Histogranin deriva
701	23	23.2	12	15	AAV48393	Histogranin deriva	774	23	23.2	15	15	AAV48389	Histogranin deriva
702	23	23.2	12	15	AAV48394	Histogranin deriva	775	23	23.2	15	15	AAV48390	Histogranin deriva
703	23	23.2	12	15	AAV48395	Histogranin deriva	776	23	23.2	15	15	AAV48391	Histogranin deriva
704	23	23.2	12	15	AAV48396	Histogranin deriva	777	23	23.2	15	15	AAV48413	Histogranin deriva
705	23	23.2	12	15	AAV48397	Histogranin deriva	778	23	23.2	15	15	AAV48416	Histogranin deriva
706	23	23.2	12	15	AAV48398	Histogranin deriva	779	23	23.2	15	15	AAV48452	Histogranin deriva
707	23	23.2	12	15	AAV48399	Histogranin deriva	780	23	23.2	15	15	AAV48455	Histogranin deriva
708	23	23.2	12	15	AAV48400	Histogranin deriva	781	23	23.2	15	15	AAV48496	Histogranin deriva
709	23	23.2	12	15	AAV48401	Histogranin deriva	782	23	23.2	15	15	AAV48497	Histogranin deriva
710	23	23.2	12	15	AAV48417	Histogranin deriva	783	23	23.2	15	15	AAV48498	Histogranin deriva
711	23	23.2	12	15	AAV48418	Histogranin deriva	784	23	23.2	15	15	AAV48499	Histogranin deriva
712	23	23.2	12	15	AAV48431	Histogranin deriva	785	23	23.2	15	15	AAV48500	Histogranin deriva
713	23	23.2	12	15	AAV48453	Histogranin deriva	786	23	23.2	15	15	AAV48502	Histogranin deriva
714	23	23.2	12	15	AAV48456	Histogranin deriva	787	23	23.2	15	15	AAV48504	Histogranin deriva
715	23	23.2	12	15	AAV48470	Histogranin deriva	788	23	23.2	15	15	AAV48505	Histogranin deriva
716	23	23.2	12	15	AAV48534	Amino terminal fra	789	23	23.2	15	15	AAV48506	Histogranin deriva
717	23	23.2	12	15	AAV48535	Amino terminal fra	790	23	23.2	15	16	AAV48537	Histogranin deriva
718	23	23.2	12	16	AAV48535	Mouse CCR-eta subu	791	23	23.2	15	19	AAV68321	Human immunodefici
719	23	23.2	12	16	AAV48535	Human HRR25-like c	792	23	23.2	15	20	AAV63057	Human secreted pro
720	23	23.2	12	16	AAV48535	Human HRR25-like c	793	23	23.2	15	21	AAV42456	Human secreted pro
721	23	23.2	12	17	AAV48535	Macrophage-colony	794	23	23.2	15	21	AAV42456	Human secreted pro
722	23	23.2	12	17	AAV48535	Macrophage-colony	795	23	23.2	15	21	AAV42456	Human secreted pro
723	23	23.2	12	17	AAV48535	Macrophage-colony	796	23	23.2	15	21	AAV42456	Human secreted pro
724	23	23.2	12	21	AAV48535	Macrophage-colony	797	23	23.2	15	21	AAV42456	Human secreted pro
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726	23	23.2	12	21	AAV48535	Macrophage-colony	799	23	23.2	15	21	AAV42456	Human secreted pro
727	23	23.2	12	21	AAV48535	Macrophage-colony	800	23	23.2	15	21	AAV42456	Human secreted pro
728	23	23.2	13	15	AAV48428	Histogranin deriva	801	23	23.2	15	21	AAV42456	Human secreted pro
729	23	23.2	13	15	AAV48467	Histogranin deriva	802	23	23.2	15	21	AAV42456	Human secreted pro
730	23	23.2	13	15	AAV48495	Histogranin deriva	803	23	23.2	15	21	AAV42456	Human secreted pro
731	23	23.2	13	20	AAV33014	Human serine prote	804	23	23.2	15	22	AAV42456	Human secreted pro
732	23	23.2	13	21	AAV16474	Human serine prote	805	23	23.2	15	22	AAV42456	Human secreted pro
733	23	23.2	13	21	AAV16474	Human serine prote	806	23	23.2	15	22	AAV42456	Human secreted pro
734	23	23.2	13	21	AAV16474	Human serine prote	807	23	23.2	15	22	AAV42456	Human secreted pro
735	23	23.2	13	22	AAV16474	Human serine prote	808	23	23.2	15	22	AAV42456	Human secreted pro
736	23	23.2	13	22	AAV16474	Human serine prote	809	23	23.2	15	22	AAV42456	Human secreted pro
737	23	23.2	13	22	AAV16474	Human serine prote	810	23	23.2	15	22	AAV42456	Human secreted pro
738	23	23.2	13	23	AAV48846	Human peptide #210	811	23	23.2	15	22	AAV48846	Human peptide #210
739	23	23.2	13	23	AAV48846	Human peptide #210	812	23	23.2	15	22	AAV48846	Human peptide #210
740	23	23.2	14	15	AAV48846	Human peptide #210	813	23	23.2	15	22	AAV48846	Human peptide #210
			</										

814	23	23.2	15	22	AAB97905	Human Casein Kinase
815	23	23.2	15	22	AAB58613	Altered MHC detern
816	23	23.2	15	23	ABJ01156	Human neurogenin 1
817	23	23.2	15	23	ABB84101	Human single chain
818	23	23.2	15	23	AAC66178	Peptide substrate
819	23	23.2	15	23	AAU78700	Peptide used in an
820	23	23.2	15	23	ABB06720	Human oestrogen re
821	23	23.2	15	23	AAM50869	Catheclin 3 antigen
822	23	23.2	16	15	AAR52095	Mouse light chain
823	23	23.2	16	15	AAR52081	Mouse light chain
824	23	23.2	16	15	AAR52082	Mouse light chain
825	23	23.2	16	15	AAR52177	Human light chain
826	23	23.2	16	15	AAR54879	Human light chain
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838	23	23.2	16	15	AAM36406	Histogranlin deriva
839	23	23.2	16	18	AAM30984	Antimicrobial prot
840	23	23.2	16	18	AAM30984	Timothy grass poll
841	23	23.2	16	21	AAV95422	Anti-angioogenic D3
842	23	23.2	16	21	AAV95423	Anti-angioogenic D3
843	23	23.2	16	21	AAV9057	Hepatitis GB virus
844	23	23.2	16	21	AAV66778	T cell antigen rec
845	23	23.2	16	23	AAE24510	Human RAR1d6 N-my
846	23	23.2	17	11	AAE24510	Human RAR1d6 N-my
847	23	23.2	17	11	AAE24510	Immunoreactive pep
848	23	23.2	17	15	AAE24510	Immunoreactive pep
849	23	23.2	17	15	AAE24510	Histogranlin deriva
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885	23	23.2	17	15	AAE24510	Histogranlin deriva
886	23	23.2	17	15	AAE24510	Histogranlin deriva

Chimeric adenovirus
Monoclonal antibody
HIV-1 p24 peptide
HIV-1 p24 peptide
TIMP-2 derived ant
Anti-colic peptide
E. coli DP3b prote
S. typhimurium DP3
Protein fragment D
Synthetic p53 pept
HIV-derived MHC cl
BAX mutant peptide
Human peptide #637
Peptide #2569 enco
Peptide #664 enco
Peptide #622 enco
Protein #2517 enco
Human brain expres
Human brain expres
Human bone marrow
Human bone marrow
Peptide #645 enco
Peptide #2547 enco
Peptide #658 enco
Peptide #2641 enco
Peptide #625 enco
Peptide #2520 enco
Rat ghrelin fragme
Anti-tetanus toxoid
Human peptide enco
Human peptide enco
Bacillus thuringiens
Helper T cell epit
Factor VIII antigen
Human p53 cellulosa
Amino acid sequen
Amino acid sequen
SRC ID NO 492 from
Human secreted p
Peptide amino acid
Human secreted p

ALIGNMENTS

XX	RESULT 1
XX	56391
XX	AAV56391 standard; peptide; 19 AA.
XX	AAV56391;
XX	15-FEB-2000 (first entry)
XX	Mutant beta-APP protein peptide sequence SEQ ID NO:1.
XX	Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;
XX	Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;
XX	gene therapy.
XX	
XX	Synthetic.
OS	Homo sapiens.
XX	
XX	MO958564-A1.
XX	
XX	18-NOV-1999.
XX	
XX	30-APR-1999; 99MO-NO00141.
XX	
XX	08-MAY-1998; 98NO-0002098.
XX	
XX	(NH2D) NORSK HYDRO AS.
XX	

PI Gaudernack G., Eriksen JA, Moller M;
XX WPI: 2000-039070/03.
DR
XX Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,
PT useful for treating Alzheimer's disease and Down syndrome -
XX
PS Claim 10; Page 27; 33pp; English.

The present invention describes frameshift mutant beta-amyloid precursor peptides (beta-APP) (AAV56391 to AAV56394) and mutant ubiquitin-B (Ubi-B) (AAV56395 to AAV56400) associated with Alzheimer's disease and Down syndrome eliciting T cellular immunity. The peptides may be used as a vaccine for Alzheimer's disease and Down syndrome. The vaccination is sufficient to induce specific T-cell immunity to mutant beta-APP and/or Ubi-B peptides that are associated with Alzheimer's disease or Down syndrome. The patient may be stimulated in vivo or ex vivo with the peptides. The peptides and DNA encoding the peptides can also be used for the treatment or prophylaxis of Alzheimer's disease or the treatment of Down syndrome.

Sequence 19 AA:

Query Match 100.0%; Score 99; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 1,6e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 NVPGHERMGRGRTSSKEIA 19
| | | | | | | | | | | | | | | | | | | | |
DB 1 NVPGHERMGRGRTSSKEIA 19

RESULT 2
AAV20219
ID AAV20219 standard; Protein; 25 AA.
XX
AC AAY20219;
XX
DT 22-JUL-1999 (first entry)

Human beta-amyloid precursor protein mutant fragment 44.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
XX frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microbulge associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
XX high mobility group protein-C; neuroendocrine specific protein A.
OS Synthetic.
OS Homo sapiens.
XX
PN WO9845322-A2
PD 15-OCT-1998.
XX
PR 02-APR-1998; 98MO-IB00705.
XX
PA 10-APR-1997; 97US-0043163.
XX
PA (UYUT-) RIJKSUNIV UTRECHT.
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
DR WPI: 1998-609901/51.
XX N-PDB: AAX5753.

PT Detecting a disease or pathological condition, associated with secretion of aberrant protein e.g. age-related diseases, by determining

WPL; 2001-397965/42.

PT Detecting a disease or pathological condition, associated with

XX Sequence 17 AA;

Query Match 52.5%; Score 52; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NVPGHERMG 9
Db 9 NVPGHERMG 17

RESULT 7
AAW18633 standard; peptide: 10 AA.

XX AAW18633;

DT 21-JUL-1997 (first entry)

XX Peptide resulting from human amyloid A4 gene +1 frameshift mutation.

XX Frameshift mutation product: GACA motif; somatic mutation; diagnosis:
XX detection; antibody; probe; cancer; neoplasia; neurodegenerative;
XX Parkinson's; Alzheimer's disease; Pick's; Huntington's disease;
XX Down's syndrome; frontal lobe dementia; progressive supranuclear palsy;
XX PSP; amyotrophic lateral sclerosis; multiple sclerosis; MS;
XX cardiovascular; rheumatoid arthritis.

OS Homo sapiens.

PN W09712992-A2.

PD 10-APR-1997.

PF 02-OCT-1996; 96MO-IB01106.

PR 11-JAN-1996; 96US-0009832.

PR 02-OCT-1995; 95GB-0020080.

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYUR-) UNIV STATE UTRECHT.

PI Burbach JPH, Grosveeld FG, Van Leeuwen FW;

DR WPI: 1997-226235/20.

PT Use of mutant genes having frameshift mutation(s) - for developing

PT prods. for the diagnosis, prevention and treatment of associated

XX diseases, e.g. cancer or neurodegenerative disease

XX Claim 24; Page 82; 123pp; English.

XX AAW18633-W18641 are antigenic peptide products of +1 and +2 frameshift
XX mutations of various human genes including the amyloid A4, tau,
XX ubiquitin, apolipoprotein E, microtubule-associated protein 2
XX (MAP-2) and neurofilament subunit L, M and H genes. The peptides
XX are used for the production of antibodies which can be used in the
XX diagnosis, prevention and treatment of diseases such as cancer or
XX neurodegenerative disease, e.g. Parkinson's disease, Alzheimer's disease
XX Down's syndrome, frontal lobe dementia (Pick's disease), progressive
XX supranuclear palsy (PSP), amyotrophic lateral sclerosis, Huntington's
XX disease, multiple sclerosis, and other degenerative diseases such as
XX cardiovascular diseases and rheumatoid arthritis.

SO Sequence 10 AA;

Query Match 47.5%; Score 47; DB 18; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 RGRSSKELA 19

Db 1 RGRSSKELA 10

RESULT 8
ID AAY20152 standard; peptide: 10 AA.

XX AAY20152;

DT 22-JUL-1999 (first entry)

XX Human beta-Ap immunogenic peptide fragment.

XX Human: beta-amyloid precursor protein; beta-Ap; diagnosis; cancer;
XX frameshift mutation; age-related disease; neurodegenerative disorder;
XX Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
XX Huntington's disease; multiple sclerosis; alcoholic liver disease;
XX diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
XX ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
XX neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
XX glial fibrillary acidic protein; GFAP; p53; semaphorin II; HUPF-1;
XX bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMG-C; NSP-A;
XX high mobility group protein-C; neuroendocrine specific protein A;
XX immunogenic.

OS Homo sapiens.

PN W09845322-A2.

PD 15-OCT-1998.

PF 02-APR-1998; 98MO-IB00705.

PR 10-APR-1997; 97US-0043163.

PA (UYUT-) RIJKSUNIV UTRECHT.

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PI Burbach JPH, Grosveeld FG, Van Leeuwen FW;

DR WPI: 1998-609901/51.

PT Diagnosing disease by detecting frameshift mutations in RNA or

PT corresponding protein mutations - used to diagnose cancer and

PT neurological diseases, particularly Alzheimer's disease, and also

PT for treatment and prevention with specific ribozymes or wild-type

XX RNA

XX Claim 24; Page 85; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease
XX caused by, or associated with, an RNA molecule that has a frameshift
XX mutation. The method is used to diagnose age-related diseases, especially
XX cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
XX disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
XX multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
XX and many others listed) or susceptibility to these disorders. The method
XX allows a definitive diagnosis of Alzheimer's disease in living patients,
XX at an early stage. It is based on the observation that disease may be
XX caused by mutations in RNA rather than DNA. The invention describes the
XX use of neuronal system RNA molecules, specifically proteins including
XX beta-amyloid precursor protein (beta-Ap), the microtubule associated
XX protein Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
XX associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
XX neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
XX protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
XX 2 (bcl-2) proto-oncogene, semaphorin II, HUPF-1, high mobility group
XX protein-C (HMGp-C) and neuroendocrine specific protein A.

SO Sequence 10 AA;

Query Match 47.5%; Score 47; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 RGRSSKELA 19
 |||||
 DB 1 RGRSSKELA 10

RESULT 9

AAB99214 ID AAB99214 standard; peptide; 10 AA.

AC AAB99214;

DT 06-SEP-2001 (first entry)

DE AMY1 peptide.

AMY1; disease detection; age-related disease; Alzheimer's disease;
 Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;
 amyotrophic lateral sclerosis; Huntington's disease; diabetes mellitus type II;
 spinocerebellar ataxia-3; multiple sclerosis; rheumatoid arthritis;
 beta-amyloid precursor protein; APP.

Unidentified.

WO200140804-A2.

PD 07-JUN-2001.

PF 04-DEC-2000; 2000WO-NL00887.

PR 03-DEC-1999; 99EP-0204140.

PA (NEW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.

PI Hol EM, Van Leeuwen FW;

DR WPI: 2001-397965/42.

PT Detecting a disease or pathological condition, associated with
 PT secretion of aberrant protein e.g. age-related diseases, by determining
 PT level of aberrant protein and/or its detectable part in body fluid
 PT and/or tissue -

XX Disclosure; Page 24; 36pp; English.

CC The present invention relates to a method for detecting a disease or
 CC pathological condition associated with molecular misreading of coding
 CC sequences in the genome and/or associated with the clearance of aberrant
 CC protein. The method comprises providing a sample of a body fluid and/or
 CC tissue of a patient and determining a level of the aberrant protein
 CC and/or its detectable part or the ratio between the two in the body fluid
 CC and/or tissue. The method enables diagnosing the disease before the
 CC patient exhibits clinical symptoms. The method is useful for diagnosing
 CC age-related diseases, preferably Alzheimer's disease, Down's syndrome or
 CC other age related diseases e.g. cancer; neurodegenerative diseases, such
 CC as frontal lobe dementia, progressive supranuclear palsy; and other
 CC diseases with abundant tau-positive filamentous lesions, Parkinson's
 CC disease, amyotrophic lateral sclerosis, Huntington's disease,
 CC spinocerebellar ataxia-3, multiple sclerosis; other inclusion body
 CC diseases associated with ubiquitin, diabetes mellitus type II and other
 CC degenerative diseases such as cardiovascular diseases and rheumatoid
 CC arthritis. A number of other diseases which can be diagnosed are given in
 CC the specification. The present sequence is AMY 1 peptide, which was
 CC coupled to thyroglobulin by glutaraldehyde, and used to immunise
 CC rabbits for antibody production in the present invention. The AMY 1
 CC peptide is a C-terminal fragment of the full-length beta-amyloid
 CC precursor protein (APP+1; mature APP and its signal peptide) protein.

XX Sequence 10 AA;

Query Match 47.5%; Score 47; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 RGRSSKELA 19
 |||||
 DB 1 RGRSSKELA 10

RESULT 10

AAV56395 ID AAV56395 standard; peptide; 15 AA.

AC AAV56395;

DT 15-FEB-2000 (first entry)

DE Mutant ubiquitin-B peptide sequence SEQ ID NO:5.

KW Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;

KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;

KW gene therapy.

OS Synthetic.

OS Homo sapiens.

PN WO958564-A1.

PD 18-NOV-1999.

PF 30-APR-1999; 99WO-N000141.

PR 08-MAY-1998; 98NO-0002098.

PA (NHVD) NORSK HYDRO AS.

PI Gaudernack G, Eriksen JA, Moller M;

DR WPI: 2000-039070/03.

PT Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,
 PT useful for treating Alzheimer's disease and Down syndrome -

XX Claim 10; Page 27; 33pp; English.

CC The present invention describes frameshift mutant beta-amyloid precursor
 CC peptides (beta-APP) (AAV56391 to AAV56394) and mutant ubiquitin-B
 CC (UBI-B) (AAV56395 to AAV56400) associated with Alzheimer's disease and
 CC Down syndrome eliciting T cellular immunity. The peptides may be used as
 CC a vaccine for Alzheimer's disease and Down syndrome. The vaccination is
 CC sufficient to induce specific T-cell immunity to mutant beta-APP and/or
 CC UBI-B peptides that are associated with Alzheimer's disease or Down
 CC syndrome. The patient may be stimulated in vivo or ex vivo with the
 CC peptides. The peptides and DNA encoding the peptides can also be used for
 CC the treatment or prophylaxis of Alzheimer's disease or the treatment of
 CC Down syndrome.

XX Sequence 15 AA;

Query Match 41.4%; Score 41; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RMGRGRTS 14
 |||||
 DB 8 RMGRGRTS 15

RESULT 11

AAAB48661 ID AAB48661 standard; peptide; 24 AA.

XX

AC AAB48661;
 XX
 DT 09-MAR-2001 (first entry).
 XX
 DE Human zvegfg4 peptide SEQ ID NO:41 used in antibody preparation.
 XX
 KW Human; zvegfg4; growth factor homologue; VEGF/PDGF family;
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic; antibody;
 KW neovascularisation; tissue repair; proliferation; differentiation;
 KW liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis;
 KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
 KW immunomodulation; hepatic.
 XX
 OS Homo sapiens.
 XX
 PN WO20006736-A1.
 XX
 PD 09-NOV-2000.
 XX
 PF 03-MAY-2000; 2000MO-US40047.
 XX
 PR 03-MAY-1999; 99US-0304216.
 XX 10-NOV-1999; 99US-0164463.
 PR 04-FEB-2000; 2000US-0180169.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gilbert T, Hart CE, Shepard PO, Gilbertson DG;
 XX
 DR WPI; 2000-687541/67.
 XX
 PT Growth factor homologs and the nucleic acids that encode them, useful
 PT e.g. for treating liver damage, ischemia, multiple sclerosis and
 PT Alzheimer's disease -
 XX
 PS Example 9; Page 72; 143pp; English.
 XX
 CC The invention relates to the human growth factor homologue zvegfg4
 CC (AAB48663), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
 CC growth factor) family. Zvegfg4 has a growth factor domain (AAB48654)
 CC characterised by a PDGF cysteine knot structure, and a CUB domain
 CC (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like
 CC activity, having mitogenic activity on fibroblasts, vascular smooth
 CC muscle cells and pericytes, and has also been shown to stimulate bone
 CC growth. The invention also relates to fusion proteins comprising human
 CC zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3
 CC fusions; expression constructs and host cells comprising human zvegfg4
 CC nucleic acids; the recombinant expression of human zvegfg4; an antibody
 CC which binds to human zvegfg4 or a fragment thereof; a method of activating
 CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a
 CC method of modulating the proliferation, differentiation, migration or
 CC metabolism of bone cells, comprising exposing bone cells to
 CC zvegfg4-derived polypeptides; and a method of detecting a genetic
 CC abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived
 CC fragments may be used to stimulate tissue development or repair, or
 CC cellular differentiation or proliferation. They are particularly used for
 CC the treatment or repair of liver damage, and may also be used to
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
 CC multiple sclerosis). Due to their osteogenic activity, they may be used
 CC in the treatment of periodontal disease and fractures. They may also be
 CC used to enhance expansion and mobilisation of haematopoietic stem cells
 CC and endothelial precursor stem cells, which may be useful in the
 CC treatment of ischemia, in wound healing, and in the modulation of the
 CC immune system. The present sequence represents a human zvegfg4 peptide
 CC used to raise antibodies in an exemplification of the invention.
 XX
 SQ Sequence 24 AA;

Query Match 33.8%; Score 33.5; DB 21; Length 24;
 Best Local Similarity 58.3%; Pred. No. 84;
 Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 3 PGH-ERMGRGT 13
 DB 4 PGHKKRRGRAKT 15

RESULT 12

AAG65607
 ID AAG65607 standard; peptide; 24 AA.

AC AAG65607;
 XX

DT 07-JAN-2002 (first entry)
 XX

DE Human zvegfg4 peptide epitope huzvegfg4-3.
 XX

KW Zvegfg4; bone; ligament; cartilage; osteoblast; osteoclast; chondrocyte;
 KW bone cancer; osteonecrosis; bone defect; osteogenesis; osteoporosis;
 KW osteopathic; vulnery; human; epitope.
 XX

OS Homo sapiens.
 XX

PN WO200157083-A1.
 XX

PD 09-AUG-2001.
 XX

PF 03-MAY-2000; 2000MO-US12095.
 XX

PR 04-FEB-2000; 2000US-180169P.
 XX 31-MAR-2000; 2000US-0540224.
 XX

PA (ZYMO) ZYMOGENETICS INC.
 XX

PI Gilbertson DG, Hart CE;
 XX

DR WPI; 2001-611088/70.
 XX

PT Use of zvegfg4 polypeptide for promoting bone, ligament or cartilage
 PT growth in mammal at site of fracture, implant, and bone graft, and for
 PT promoting growth or differentiation of osteoblasts, chondrocytes in
 PT culture -
 XX
 PS Example 3; Page 23; 57pp; English.
 XX

CC The invention relates to the use of zvegfg4 polypeptide for promoting
 CC bone, ligament or cartilage growth in a mammal, and for promoting
 CC proliferation or differentiation of osteoblasts, osteoclasts,
 CC chondrocytes or bone marrow stem cells in culture. For promoting
 CC cartilage growth, chondrocytes are cultured ex vivo in presence of the
 CC zvegfg4 polypeptide and then placed into mammal where cartilage is to be
 CC grown. Zvegfg4 polypeptide is useful for promoting growth of bone,
 CC ligament or cartilage in a mammal at a site of bony defect such as
 CC fracture, bone graft, implant or periodontal pocket, in humans and non-
 CC human animals such as domestic animals including livestock and companion
 CC animals. Zvegfg4 is used for promoting growth of bone, ligament, or
 CC cartilage in conditions of bone defects following therapeutic treatments
 CC of bone cancers or other conditions characterized by increased bone loss
 CC or decreased bone formation, or elevation of peak bone mass in pre-
 CC menopausal woman. It is also useful for healing bone following radiation
 CC -induced osteonecrosis, repairing bone defects arising from surgery, and
 CC promotion of bone healing in plastic surgery, increasing bone formation
 CC during distraction osteogenesis, treating bone injuries including repair
 CC of cartilage and ligament and treatment of osteoporosis. Sequences
 CC AAG65605-07 represents peptide epitopes of human zvegfg4 polypeptide,
 CC used for raising rabbit polyclonal antibodies.
 XX

SQ Sequence 24 AA;

Query Match 33.8%; Score 33.5; DB 22; Length 24;
 Best Local Similarity 58.3%; Pred. No. 84;
 Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
 OY 3 PGH-ERMGRGT 13
 III : I I I I I

CC Probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC

Sequence 20 AA:

Query Match 33.3%; Score 33; DB 22; Length 20;
 Best Local Similarity 58.3%; Pred. No. 85;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 8 MGRGRTSSKELA 19
 :||||| ||: |
 Db 5 VGRGRHCSKRTA 16

RESULT 15
 ABB35121
 ID ABB35121 standard; Peptide: 20 AA.

AC ABB35121;

DE 04-FEB-2002 (first entry)

PE Peptide #2627 encoded by human foetal liver single exon probe.

Human: foetal liver; gene expression: single exon nucleic acid probe.

Homo sapiens.

WO200157277-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00669.

04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI: 2001-483447/52.

Human genome-derived single exon nucleic acid probes useful for

analyzing gene expression in human fetal liver -

Claim 27; SEQ ID NO 27756; 639pp + sequence listing; English.

The invention relates to a single exon nucleic acid probe for

measuring human gene expression in a sample derived from human foetal

liver. The single exon nucleic acid probes may be used for predicting,

measuring and displaying gene expression in samples derived from human

fetal liver. The present sequence is a peptide encoded by a single exon

nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the

printed specification, but was obtained in electronic format directly

from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Db 5 VGRGRHCSKRTA 16

RESULT 16

AAM55944
 ID AAM55944 standard; Protein: 20 AA.

AC AAM55944;

DE 05-NOV-2001 (first entry)

Human brain expressed single exon probe encoded protein SEQ ID NO: 28049.

Human: brain expressed exon; gene expression analysis; probe:

microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

epilepsy; cancer.

Homo sapiens.

WO200157275-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00667.

04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI: 2001-483446/52.

Single exon nucleic acid probes for analyzing gene expression in human

brains -

Example 4; SEQ ID NO: 28049; 650pp + sequence listing; English.

The present invention provides a number of single exon nucleic acid

probes which are derived from genomic sequences expressed in the human

brain. They can be used to measure gene expression in brain cell samples,

which may enable the diagnosis and improved treatment of nervous system

diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

epilepsy and cancers. The present sequence is a protein encoded by one of

the probes of the invention.

Sequence 20 AA:

Query Match 33.3%; Score 33; DB 22; Length 20;

Best Local Similarity 58.3%; Pred. No. 85;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 8 MGRGRTSSKELA 19

:||||| ||: |

Db 5 VGRGRHCSKRTA 16

RESULT 17

AAM68310

ID AAM68310 standard; Protein: 20 AA.

AC AAM68310;

DE 06-NOV-2001 (first entry)

Human bone marrow expressed probe encoded protein SEQ ID NO: 28616.

KW Human; bone marrow expressed exon; gene expression analysis; probe;
KM microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX WO200157276-A2.
XX
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00668.
XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
XX PS Example 4; SEQ ID NO: 28616; 658bp + Sequence Listing; English.
XX
XX CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention.
XX
XX SQ Sequence 20 AA:

Query Match 33.3%; Score 33; DB 22; Length 20;
Best Local Similarity 58.3%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 8 MGRGRTSKELA 19
:|||||::|
Db 5 VGRGRHCKKTA 16

RESULT 18
ID AAM03860 standard; Protein: 20 AA.
XX
XX AC AAM03860;
XX
XX DT 09-OCT-2001 (first entry)
XX
XX DE Peptide #2542 encoded by probe for measuring breast gene expression.
XX
XX KW Probe; human; breast disease; breast cancer; development disorder;
KM inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX OS Homo sapiens.
XX
XX PN WO200157270-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 29-JAN-2001; 2001WO-US00661.
XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX DR WPI; 2001-476286/51.
XX
XX PT Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX
XX PS Claim 27; SEQ ID NO 12600; 322pp; English.
XX
XX CC The present invention relates to novel single exon nucleic acid probes
CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer, disorders of development,
CC inflammatory diseases of the breast, fibrocystic changes, proliferative
CC breast disease and non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 20 AA:

Query Match 33.3%; Score 33; DB 22; Length 20;
Best Local Similarity 58.3%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 8 MGRGRTSKELA 19
:|||||::|
Db 5 VGRGRHCKKTA 16

RESULT 19
ID ABG37860 standard; Peptide: 20 AA.
XX
XX AC ABG37860;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 27525.
XX
XX DE Human; single exon probe; asthma; lung cancer; COPD; ILD;
KM chronic obstructive pulmonary disease; interstitial lung disease;
KM familial idiopathic pulmonary fibrosis; neurofibromatosis;
KM tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
KM Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KM pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KM primary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KM primary ciliary dyskinesia; pulmonary hypertension;
KM hyaline membrane disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200186003-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00665.
XX
XX PR 04-FEB-2000; 2000US-180312P.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-234687P.

CC The proteins are useful in the diagnosis, detection and treatment of
CC diseases and/or disorders associated with aberrant uteroglobin-like
CC activity, such as inflammatory disorders (glomerulonephritis, rheumatoid
CC arthritis, autoimmune disorders e.g., multiple sclerosis, Grave's
CC disease), respiratory disorders (allergy, asthma); immune deficiency
CC diseases (leukemia, sepsis, acne, psoriasis); cancers (adenocarcinoma);
CC gastrointestinal disorders (inflammatory bowel disease); immunologic
CC deficiency syndromes (DiGeorge syndrome, HIV infection); haematopoietic
CC disorders, transplantation rejections (graft-versus-host disease);
CC hyperproliferative disorders (neoplasm, Gaucher's disease);
CC cardiovascular diseases (arrhythmias); cerebrovascular diseases
CC (thrombosis), sex-linked disorders, for treating infectious agents,
CC tumours, uveitis, atherosclerosis, ulcers, as birth control agent, wound
CC healing, and for treating neurodegenerative and behavioural disorders
CC (e.g., Alzheimer's disease, Parkinson's disease, Hartung disease, mania,
CC autism). Uteroglobin-like proteins and antibodies are useful as reagents
CC for differential identification of tissues or cell types present in a
CC biological sample. They are also used as immunological probes for
CC differential identification of tissues. The polynucleotides of the
CC invention are useful in gene therapy, for chromosome identification.
CC The present sequence represents a human uteroglobin-like protein HFCB041
CC fragment of the invention.

SQ Sequence 17 AA;

Query Match 32.3%; Score 32; DB 22; Length 17;

Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;OY 3 PGERMGRG 11
1 1 1 1 1
DB 9 PHEHMLPG 17

RESULT 24

AAR04485

ID: AAR04485 standard; protein: 18 AA.

XX AAR04485;

XX 20-SEP-1990 (first entry)

XX Human immunodeficiency virus hybrid peptide RP113.

XX Hybrid peptide RP113; therapy; AIDS; principal neutralising domain;

XX antibodies; diagnosis; prophylaxis.

XX Synthetic.

XX WO9003984-A.

XX 19-APR-1990.

XX 29-SEP-1989; 89WO-US04302.

XX 19-SEP-1989; 89US-0407663, US-252949; WO-U04302.

XX (REPL-) REPLIGEN CORP.

XX Rusche JR, Putney SD, Javaherian K, Farley J, Grimalia R, Lynn D;
XX Petro-Breyer J;

XX WPI: 1990-147824/19.

XX Principal neutralising domain of HIV variants - used for producing
XX peptide(s) and antibodies for diagnosis; prophylaxis; and/or therapy
XX of HIV infection.

XX Claim 8 (88); Page 77; 108pp; English.

XX Peptide RP113 comprises segments of the Principal Neutralising Domain
XX (envelope protein) from a HIV isolate.
XX The last Cys residue is added for the purpose of crosslinking

CC to carrier proteins. Cysteine residues may be added, so that the
CC residues at or near both ends form a disulfide bond, giving peptide a
CC loop-like configuration, which can be utilised to enhance immunogenic
CC properties of the peptides. Protein is capable of eliciting, and/or
CC binding with, neutralising antibodies. The neutralising domain is bounded
CC by cysteine residues which occur at positions 296 and 331. The peptides
CC can be used as immunogens or screening reagents to generate or identify
CC poly- or monoclonal antibodies.
CC See also AAR04427-R04506 and AAR04273-Q04279.

SQ Sequence 18 AA;

Query Match 32.3%; Score 32; DB 11; Length 18;

Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;OY 3 PGERMGRGR 12
1 1 1 1 1 1
DB 4 PGRHPRGR 13

RESULT 25

AAM72540

ID: AAM72540 standard; protein: 19 AA.

XX AAM72540;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 32846.

XX Human; bone marrow expressed exon; gene expression analysis; probe;

XX microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI: 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX Example 4; SEQ ID NO: 32846; 658bp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention.

SQ Sequence 19 AA;

Query Match 32.3%; Score 32; DB 22; Length 19;

Best Local Similarity 46.2%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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OY 3 PGHERMGRRSS 15
| | : | | | |
Db 3 FOHRHLEGLDSS 15

Search completed: March 14, 2003, 16:05:44
job time : 54 secs